GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 15:53:35 ; Search time 1221 Seconds
(without alignments)
1708.756 Million cell updates/sec

Title: US-09-856-937A-1_COPY_580_630
Perfect score: 51
Sequence: 1 agcagaggcagcgagttggg.....ctgccatggtgtgtccctct 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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14: gb_vi:*
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34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		51	100.0	870	11	G15915	G15915 human STS C
2		51	100.0	2224	6	AR152033	AR152033 Sequence
3		51	100.0	2224	6	AR308134	AR308134 Sequence
4		51	100.0	2253	6	A78517	A78517 Sequence 1
5		51	100.0	2613	9	HSTNFR2S10	U52165 Human tumor
6		51	100.0	3380	11	G26865	G26865 human STS S
7		51	100.0	3683	6	AR215688	AR215688 Sequence
8		51	100.0	3683	6	AX333705	AX333705 Sequence
9		51	100.0	3683	6	AX348016	AX348016 Sequence
10		51	100.0	3683	6	AX348018	AX348018 Sequence
11		51	100.0	3683	6	AX348020	AX348020 Sequence
12		51	100.0	3683	6	AX698020	AX698020 Sequence
13		51	100.0	3683	9	HUMNFR	M32315 Human tumor
14		49.4	96.9	2282	9	BC042167	BC042167 Homo sapi
15		49.4	96.9	3692	9	BC052977	BC052977 Homo sapi
16		47.8	93.7	2339	6	A26415	A26415 cDNA fragme
17		47.8	93.7	2394	9	HUMTNFRII	M55994 Human tumor
18		47.8	93.7	3492	9	S63368	S63368 Homo sapien
19		47.8	93.7	15602	6	AR215702	AR215702 Sequence
20		47.8	93.7	45584	9	AY264804	AY264804 Homo sapi
c 21		47.8	93.7	115602	9	HS1118D24	AL031276 Human DNA
22		47.8	93.7	122105	2	AL355998	AL355998 Homo sapi
23		47.8	93.7	153904	2	BX510650	BX510650 Homo sapi
24		47.8	93.7	187877	2	AC023251	AC023251 Homo sapi
c 25		30.4	59.6	139958	2	AC141936	AC141936 Rattus no
26		28.8	56.5	212202	2	AC137977	AC137977 Mus muscu
27		26.8	52.5	187783	2	AC137462	AC137462 Rattus no
c 28		26.8	52.5	267375	2	AC095339	AC095339 Rattus no
29		26.6	52.2	104762	2	AC108086	AC108086 Homo sapi
c 30		26.6	52.2	155666	9	AC008696	AC008696 Homo sapi
c 31		26.6	52.2	174640	2	AC024479	AC024479 Homo sapi
32		26.6	52.2	187478	2	AC123758	AC123758 Mus muscu
33		26.6	52.2	231407	2	AC139592	AC139592 Rattus no
34		26.4	51.8	303230	2	AC112836	AC112836 Rattus no
c 35		26.2	51.4	218935	2	AC102660	AC102660 Mus muscu
36		26	51.0	184541	2	AC118696	AC118696 Mus muscu
37		26	51.0	234681	2	AC095940	AC095940 Rattus no
38		25.8	50.6	59192	2	AC101314	AC101314 Mus muscu
c 39		25.8	50.6	220147	2	AC113524	AC113524 Mus muscu
c 40		25.6	50.2	91745	9	AC009297	AC009297 Homo sapi
c 41		25.6	50.2	100000	9	AP000010	AP000010 Homo sapi
c 42		25.6	50.2	100000	9	AP000151	AP000151 Homo sapi
c 43		25.6	50.2	102247	9	AP001432	AP001432 Homo sapi
c 44		25.6	50.2	227682	2	AC131460	AC131460 Rattus no
c 45		25.6	50.2	340000	9	AP001728	AP001728 Homo sapi

ALIGNMENTS

RESULT 1
G15915
LOCUS G15915 870 bp DNA linear STS 19-JAN-1996
DEFINITION human STS CHLC.UTR_02819_M32315.P65016 clone UTR_02819_M32315, sequence tagged site.
ACCESSION G15915
VERSION G15915.1 GI:1161804
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H.
TITLE Cooperative Human Linkage Center

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  JOURNAL   Unpublished (1995)
COMMENT     Synonyms: UTR_02819_M32315, CHLC.UTR_02819_M32315.T36190
            Contact: Dr. Jeffrey C. Murray
            UofI
            The University of Iowa
            Department of Pediatrics, Iowa City, IA 52242, USA
            Tel: (319) 356-3508
            Fax: (319) 356-3347
            Email: jeff-murray@uiowa.edu

            Primer A: CCCTGACTCTCTGTGACCTG
            Primer B: GTCTTCATGGGTGACTCAGG
            STS size: 206
            PCR Profile:
                        denature:    30 seconds at 94 degrees C
                        annealing:   75 seconds at 55 degrees C
                        extension:   15 seconds at 72 degrees C
                        PCR cycles:  27
                        extension:    6 minutes at 72 degress C
            Protocol:
                        Template:        30ng genomic DNA
                        Primer:          each 1.5 pmole
                        dNTPs:           each 200 uM
                        Taq Polymerase:  0.3 units
                        Total Vol:       10 ul

            Buffer:
                        MgCl2:  1.5mM
                        KCl:     50mM
                        Tris:    10mM
                        pH:     8.3

                        Prepared with primer pairs derived from M32315.
FEATURES              Location/Qualifiers
     source           1. .870
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
     STS              272. .477
     primer_bind      272. .291
     primer_bind      complement(458. .477)
BASE COUNT      157 a    246 c    279 g    188 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 11;  Length 870;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 225


RESULT 2
AR152033
LOCUS       AR152033                2224 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6232446.
ACCESSION   AR152033
VERSION     AR152033.1  GI:15118083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2224)
  AUTHORS   Wallach,D., Bigda,J., Beletsky,I., Mett,I. and Engelmann,H.
  TITLE     TNF ligands
  JOURNAL   Patent: US 6232446-A 2 15-MAY-2001;
FEATURES              Location/Qualifiers
     source           1. .2224
                      /organism="unknown"
BASE COUNT      435 a    698 c    689 g    402 t
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  Best Local Similarity   100.0%;  Pred. No. 9e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 3
AR308134
LOCUS       AR308134                2224 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6555111.
ACCESSION   AR308134
VERSION     AR308134.1  GI:31699179
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2224)
  AUTHORS   Wallach,D., Bigda,J., Beletsky,I., Mett,I. and Engelmann,H.
  TITLE     Method of inhibiting the cytocidal effect of TNF with TNF
            receptor-specific antibodies
  JOURNAL   Patent: US 6555111-A 1 29-APR-2003;
FEATURES              Location/Qualifiers
     source           1. .2224
                      /organism="unknown"
BASE COUNT      435 a    698 c    689 g    402 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 2224;
  Best Local Similarity   100.0%;  Pred. No. 9e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 4
A78517
LOCUS       A78517                  2253 bp    DNA     linear   PAT 19-OCT-1999
DEFINITION  Sequence 1 from Patent EP0585939.
ACCESSION   A78517
VERSION     A78517.1  GI:6090179
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2253)
  AUTHORS   Mett,I. and Wallach,D.
  TITLE     TNF LIGANDS
  JOURNAL   Patent: EP 0585939-A 1 09-MAR-1994;
            YEDA RES & DEV (IL)
FEATURES              Location/Qualifiers
     source           1. .2253
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
     CDS              90. .1475
                      /note="unnamed protein product"
                      /codon_start=1
                      /protein_id="CAB58915.1"
                      /db_xref="GI:6090180"
                      /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
                      YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
                      DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV
                      CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
                      PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                      GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                      ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                      HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                      LGVPDAGMKPS"
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BASE COUNT      440 a    709 c    698 g    406 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 2253;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 5
HSTNFR2S10
LOCUS       HSTNFR2S10              2613 bp    DNA     linear   PRI 31-JUL-1996
DEFINITION  Human tumor necrosis factor receptor 2 (TNFR2) gene, exon 10 and
            complete cds.
ACCESSION   U52165
VERSION     U52165.1  GI:1469539
KEYWORDS    .
SEGMENT     10 of 10
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2613)
  AUTHORS   Beltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
            LePaslier,D., Stallard,B.J., Goeddel,D.V., de Sauvage,F.J. and
            Brodeur,G.M.
  TITLE     Physical mapping and genomic structure of the human TNFR2 gene
  JOURNAL   Genomics 35 (1), 94-100 (1996)
  MEDLINE   96299745
   PUBMED   8661109
REFERENCE   2  (bases 1 to 2613)
  AUTHORS   Beltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
            LePaslier,D., Stallard,B.J., Goeddel,D.V., deSauvage,F.J. and
            Brodeur,G.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAR-1996) Christian P. Beltinger, Division of
            Oncology, ARC Rm. 902 D, Childrens's Hospital of Philadelphia, 324
            South 34th Street, Philadelphia, PA 19104-4318, USA
FEATURES             Location/Qualifiers
     source          1. .2613
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1p36.2"
     mRNA            join(U52156.1:1. .167,U52157.1:7. .106,U52158.1:114. .242,
                     U52159.1:7. .156,U52160.1:7. .100,U52161.1:95. .330,
                     U52162.1:83. .160,U52163.1:7. .41,U52164.1:7. .211,125. .2613)
                     /product="tumor necrosis factor receptor"
     CDS             join(U52156.1:90. .167,U52157.1:7. .106,U52158.1:114. .242,
                     U52159.1:7. .156,U52160.1:7. .100,U52161.1:95. .330,
                     U52162.1:83. .160,U52163.1:7. .41,U52164.1:7. .211,125. .405)
                     /codon_start=1
                     /product="tumor necrosis factor receptor"
                     /protein_id="AAC50622.1"
                     /db_xref="GI:1469541"
                     /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
                     YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
                     DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV
                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                     ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
     gene            join(U52157.1:7. .112,U52158.1:1. .248,U52159.1:1. .200,
                     U52160.1:1. .106,U52161.1:1. .336,U52162.1:1. .218,
                     U52163.1:1. .58,U52164.1:1. .234,1. .2613)
                     /gene="TNFR2"
     intron          <1. .124
                     /gene="TNFR2"
                     /number=9
     exon            125. .2613
                     /gene="TNFR2"
                     /number=10
BASE COUNT      553 a    750 c    742 g    568 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 9;  Length 2613;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db        580 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 630


RESULT 6
G26865
LOCUS       G26865                  3380 bp    DNA     linear   STS 14-JUN-1996
DEFINITION  human STS SHGC-31494, sequence tagged site.
ACCESSION   G26865
VERSION     G26865.1  GI:1375115
KEYWORDS    STS; STS sequence; primer; sequence tagged site.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3380)
  AUTHORS   Myers,R.M.
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Richard M. Myers
            Stanford Human Genome Center (SHGC)
            Stanford University School of Medicine
            Department of Genetics, M-344, Stanford, CA 94305, USA
            Tel: 4157259687
            Fax: 4157259689
            Email: myers@shgc.stanford.edu

            Primer A: CCCCACCACTAGGACTCTGA
            Primer B: CACAGAGAGTCAGGGACTTGC
            STS size: 201
            PCR Profile:
                    Initial incubation: 94 degrees C for 90 seconds

                    Denaturation:       94 degrees C for 15 seconds
                    Annealing:          62 degrees C for 23 seconds
                    Polymerization:     72 degrees C for 30 seconds
                    PCR Cycles:         30
                    Thermal Cycler:     Perkin Elmer 9600
            Protocol:
                    Template:       25 ng
                    Primer:         each 1 uM
                    dNTPs:          each 200 uM
                    Taq Polymerase: 0.05 units/ul
                    Total Vol:      10 ul

            Buffer:
                    MgCl2:          2.5 mM
                    KCl:            50  mM
                    Tris-HCl:       20  mM
                    pH:             8.3

            Prepared with primer pairs provided by Sandoz, derived from M32315
            -- Washington University/Merck EST sequence.
FEATURES             Location/Qualifiers
     source          1. .3380
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="1"
     STS             1561. .1761
```

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     primer_bind     1561. .1580
     primer_bind     complement(1741. .1761)
BASE COUNT      703 a   1029 c   1004 g    644 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 8.7e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 7
AR215688
LOCUS       AR215688               3683 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 3 from patent US 6410324.
ACCESSION   AR215688
VERSION     AR215688.1  GI:23313944
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3683)
  AUTHORS   Bennett,C.F. and Watt,A.T.
  TITLE     Antisense modulation of tumor necrosis factor receptor 2 expression
  JOURNAL   Patent: US 6410324-A 3 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .3683
                     /organism="unknown"
BASE COUNT      781 a   1098 c   1086 g    718 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 8
AX333705
LOCUS       AX333705               3683 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 4214 from Patent WO0194629.
ACCESSION   AX333705
VERSION     AX333705.1  GI:18124424
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 4214 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 8.6e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 9
AX348016
LOCUS       AX348016               3683 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 49 from Patent EP1172444.
ACCESSION   AX348016
VERSION     AX348016.1  GI:18614126
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schreiber,S., Hampe,J. and Mascheretti,S.
  TITLE     Diagnostic use of polymorphisms in the gene coding for the tnf
            receptor II and method for detecting non-responders to anti-tnf
            therapy
  JOURNAL   Patent: EP 1172444-A 49 16-JAN-2002;
            Conaris Research Institute GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .3683
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS             90. .1475
                     /note="unnamed protein product"
                     /codon_start=1
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                     YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
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                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
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                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
     mat_peptide     156
BASE COUNT      781 a   1098 c   1086 g    718 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 10
AX348018
LOCUS       AX348018               3683 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 51 from Patent EP1172444.
ACCESSION   AX348018
VERSION     AX348018.1  GI:18614128
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schreiber,S., Hampe,J. and Mascheretti,S.
  TITLE     Diagnostic use of polymorphisms in the gene coding for the tnf
            receptor II and method for detecting non-responders to anti-tnf
            therapy
  JOURNAL   Patent: EP 1172444-A 51 16-JAN-2002;
            Conaris Research Institute GmbH (DE)
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FEATURES             Location/Qualifiers
     source          1. .3683
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS             90. .1475
                     /note="unnamed protein product"
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                     /db_xref="GI:18614129"
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                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
     mat_peptide     156
BASE COUNT      780 a   1098 c   1087 g    718 t
ORIGIN

  Query Match           100.0%;  Score 51;  DB 6;  Length 3683;
  Best Local Similarity  100.0%;  Pred. No. 8.6e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 11
AX348020
LOCUS       AX348020               3683 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 53 from Patent EP1172444.
ACCESSION   AX348020
VERSION     AX348020.1  GI:18614130
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schreiber,S., Hampe,J. and Mascheretti,S.
  TITLE     Diagnostic use of polymorphisms in the gene coding for the tnf
            receptor II and method for detecting non-responders to anti-tnf
            therapy
  JOURNAL   Patent: EP 1172444-A 53 16-JAN-2002;
            Conaris Research Institute GmbH (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /note="unnamed protein product"
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                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASRDAVCTSTSPTRSMAPGAVHLPQ
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                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                     ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
     mat_peptide     156
BASE COUNT      780 a   1098 c   1088 g    717 t
ORIGIN

  Query Match           100.0%;  Score 51;  DB 6;  Length 3683;
  Best Local Similarity  100.0%;  Pred. No. 8.6e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 12
AX698020
LOCUS       AX698020               3683 bp    DNA     linear   PAT 02-APR-2003
DEFINITION  Sequence 1 from Patent WO03009864.
ACCESSION   AX698020
VERSION     AX698020.1  GI:29499058
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lucas,J., Dialynas,D., Briggs,K. and Scalia,A.
  TITLE     Agonists and antagonists of disomet for the treatment of metabolic
            disorders
  JOURNAL   Patent: WO 03009864-A 1 06-FEB-2003;
            GENSET SA (FR)
FEATURES             Location/Qualifiers
     source          1. .3683
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
     5'UTR           1. .89
     CDS             90. .1475
                     /note="unnamed protein product"
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                     /protein_id="CAD87412.1"
                     /db_xref="GI:29499059"
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                     LGVPDAGMKPS"
     3'UTR           1476. .3657
     polyA_signal    3658. .3663
BASE COUNT      781 a   1098 c   1086 g    718 t
ORIGIN

  Query Match           100.0%;  Score 51;  DB 6;  Length 3683;
  Best Local Similarity  100.0%;  Pred. No. 8.6e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 13
HUMNFR
LOCUS       HUMNFR                 3683 bp    mRNA    linear   PRI 07-JAN-1995
DEFINITION  Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M32315
VERSION     M32315.1  GI:189185
KEYWORDS    c-myc proto-oncogene; necrosis factor receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3683)
  AUTHORS   Smith,C.A., Davis,T., Anderson,D., Solam,L., Beckmann,M.P.,
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            Jerzy,R., Dower,S.K., Cosman,D. and Goodwin,R.G.
  TITLE     A receptor for tumor necrosis factor defines an unusual family of
            cellular and viral proteins
  JOURNAL   Science 248 (4958), 1019-1023 (1990)
  MEDLINE   90260639
   PUBMED   2160731
COMMENT     Original source text: Homo sapiens lung cDNA to mRNA.
            Draft entry and computer-readable sequence for [1] kindly submitted
            by C.A.Smith, 30-MAR-1990, for release after publication.
FEATURES             Location/Qualifiers
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                     /cell_line="WI26-VA4"
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     gene            1. .3683
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     CDS             90. .1475
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BASE COUNT      781 a   1098 c   1086 g    718 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 9;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 14
BC042167
LOCUS       BC042167                2282 bp    mRNA    linear   PRI 09-JAN-2003
DEFINITION  Homo sapiens, Similar to tumor necrosis factor receptor
            superfamily, member 1B, clone IMAGE:5022068, mRNA, partial cds.
ACCESSION   BC042167
VERSION     BC042167.1  GI:27503828
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2282)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JAN-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 44 Row: h Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 23312365.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5022068"
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                     /clone_lib="NIH_MGC_17"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     CDS             <1. .1375
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                     /protein_id="AAH42167.1"
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BASE COUNT      459 a    706 c    708 g    409 t
ORIGIN

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  Best Local Similarity   98.0%;  Pred. No. 3.7e-08;
  Matches   50;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db       1550 AGCAGAGGCAGCGAGTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1600


RESULT 15
BC052977
LOCUS       BC052977                3692 bp    mRNA    linear   PRI 09-JUN-2003
DEFINITION  Homo sapiens tumor necrosis factor receptor superfamily, member 1B,
            mRNA (cDNA clone MGC:60023 IMAGE:6198614), complete cds.
ACCESSION   BC052977
VERSION     BC052977.1  GI:31419789
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3692)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
```

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 3692)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (02-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 110 Row: n Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23312365.

FEATURES Location/Qualifiers

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gene 1. .3692
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CDS 88. .1473
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BASE COUNT 791 a 1098 c 1085 g 718 t

ORIGIN

Query Match 96.9%; Score 49.4; DB 9; Length 3692;
Best Local Similarity 98.0%; Pred. No. 3.6e-08;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Job time : 1225 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
919.531 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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12: gb_est3:*
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14: gb_est5:*
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16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	49.4	96.9	372	9	AA031826	AA031826 zk14b11.r
c	2	49.4	96.9	735	14	CA426262	CA426262 UI-H-DF0-
	3	49.4	96.9	2291	11	BC011844	BC011844 Homo sapi
	4	47.8	93.7	760	12	BI161017	BI161017 602865227
	5	47.8	93.7	932	12	BG829828	BG829828 602764119
	6	47.8	93.7	974	10	BG745202	BG745202 602723532
	7	47.8	93.7	1051	10	BF568409	BF568409 602184408
c	8	47.8	93.7	1053	12	BQ052282	BQ052282 AGENCOURT
	9	47.8	93.7	1102	12	BM917316	BM917316 AGENCOURT
c	10	35.2	69.0	1183	10	BF569011	BF569011 602184353
	11	31.8	62.4	472	9	AV746487	AV746487 AV746487
	12	28.6	56.1	945	13	BX327945	BX327945 BX327945
	13	26.8	52.5	150	9	AW176594	AW176594 RC5-CT007
	14	26.8	52.5	175	9	AW062603	AW062603 RC0-CT008
	15	26.8	52.5	689	28	BZ092262	BZ092262 CH230-232
c	16	26.6	52.2	765	12	BI102359	BI102359 602888005
c	17	26.6	52.2	794	10	BF540303	BF540303 602052359
c	18	26.4	51.8	368	13	BY500376	BY500376 BY500376
c	19	26.4	51.8	431	13	BY501435	BY501435 BY501435
c	20	26.4	51.8	446	13	BY474057	BY474057 BY474057
c	21	26.4	51.8	478	10	BB781904	BB781904 BB781904
c	22	26.4	51.8	685	10	BG077751	BG077751 H3019C10-
	23	26.4	51.8	1066	10	BF568708	BF568708 602184353
	24	26	51.0	333	28	AZ398572	AZ398572 1M0164H05
c	25	26	51.0	428	13	BY432020	BY432020 BY432020
c	26	26	51.0	880	13	BU176729	BU176729 AGENCOURT
	27	25.6	50.2	383	13	BY007173	BY007173 BY007173
	28	25.6	50.2	562	28	AQ470055	AQ470055 CITBI-E1-
c	29	25.4	49.8	355	13	BY397944	BY397944 BY397944
c	30	25.4	49.8	377	10	AW938801	AW938801 PM0-DT006
c	31	25.4	49.8	400	13	BY404734	BY404734 BY404734
c	32	25	49.0	337	9	AW801622	AW801622 IL5-UM006
c	33	25	49.0	369	12	BM448184	BM448184 DSA015D12
c	34	25	49.0	413	12	BM780538	BM780538 APL1_4_H0
c	35	25	49.0	439	13	BY432386	BY432386 BY432386
	36	25	49.0	475	10	BB759149	BB759149 BB759149
c	37	25	49.0	533	9	AI155645	AI155645 ue06a09.r
	38	25	49.0	728	28	BH898693	BH898693 MB61p10C4
	39	25	49.0	845	12	BI160187	BI160187 602864057
c	40	24.8	48.6	203	9	AA795560	AA795560 vq96g12.r
c	41	24.8	48.6	318	9	AA959223	AA959223 ua10h05.r
c	42	24.8	48.6	323	9	AA218140	AA218140 mv61d01.r
c	43	24.8	48.6	346	10	BF771882	BF771882 IL5-IT002
	44	24.8	48.6	347	9	AI840820	AI840820 UI-M-AH0-
c	45	24.8	48.6	351	14	W16081	W16081 mb60h02.r1

ALIGNMENTS

RESULT 1
AA031826
LOCUS AA031826 372 bp mRNA linear EST 09-MAY-1997
DEFINITION zk14b11.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:470493 5' similar to gb:M32315 TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (HUMAN);contains element PTR5 repetitive element ;, mRNA sequence.
ACCESSION AA031826
VERSION AA031826.1 GI:1501789
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 372)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549
COMMENT Contact: Wilson RK
Washington University School of Medicine

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           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: est@watson.wustl.edu
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           Insert Length: 849   Std Error: 0.00
           Seq primer: -28M13 rev2 from Amersham
           High quality sequence stop: 362.
FEATURES             Location/Qualifiers
     source          1. .372
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:3756495"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:470493"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="Soares_pregnant_uterus_NbHPU"
                     /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization.  Library
                     constructed by M. Fatima Bonaldo."
BASE COUNT       51 a    122 c    102 g     97 t
ORIGIN

  Query Match             96.9%;  Score 49.4;  DB 9;  Length 372;
  Best Local Similarity   98.0%;  Pred. No. 4.4e-06;
  Matches   50;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        118 AGCAGAGGCAGCGAGTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 168


RESULT 2
CA426262/c
LOCUS       CA426262                735 bp    mRNA    linear   EST 07-NOV-2002
DEFINITION  UI-H-DF0-bek-n-21-0-UI.s1 NCI_CGAP_DF0 Homo sapiens cDNA clone
            UI-H-DF0-bek-n-21-0-UI 3', mRNA sequence.
ACCESSION   CA426262
VERSION     CA426262.1  GI:24788988
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 11-300, >ALU (matched compliment) 539-573, >(CAAA
            )n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-DF0-bek-n-21-0-UI"
                     /tissue_type="Subchondral Bone"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_DF0"
                     /note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_DF0 is a cDNA library containing the following
                     tissue(s): Subchondral Bone. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is GTTAAGCGTC.
                     TAG_LIB=UI-H-DF0
                     TAG_TISSUE=subchondral bone
                     TAG_SEQ=GTTAAGCGTC"
BASE COUNT      159 a    231 c    191 g    153 t      1 others
ORIGIN

  Query Match             96.9%;  Score 49.4;  DB 14;  Length 735;
  Best Local Similarity   98.0%;  Pred. No. 5.7e-06;
  Matches   50;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        735 AGCAGAGGCAGCGAGTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 685


RESULT 3
BC011844
LOCUS       BC011844                2291 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, Similar to tumor necrosis factor receptor
            superfamily, member 1B, clone IMAGE:4111730, mRNA.
ACCESSION   BC011844
VERSION     BC011844.1  GI:15080140
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2291)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUL-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
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            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 28 Row: i Column: 15
            This clone has the following problem: retained intron.
FEATURES              Location/Qualifiers
     source           1. .2291
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4111730"
                      /tissue_type="Muscle, rhabdomyosarcoma"
                      /clone_lib="NIH_MGC_17"
                      /lab_host="DH10B-R"
                      /note="Vector: pOTB7"
BASE COUNT      461 a    708 c    713 g    409 t
ORIGIN

  Query Match             96.9%;  Score 49.4;  DB 11;  Length 2291;
  Best Local Similarity   98.0%;  Pred. No. 8.9e-06;
  Matches   50;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1559 AGCAGAGGCAGCGAGTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1609


RESULT 4
BI161017
LOCUS       BI161017                760 bp    mRNA    linear   EST 05-JUL-2001
DEFINITION  602865227F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019247 5',
            mRNA sequence.
ACCESSION   BI161017
VERSION     BI161017.1  GI:14621018
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 760)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1834  row: e  column: 08
            High quality sequence stop: 723.
FEATURES              Location/Qualifiers
     source           1. .760
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5019247"
                      /tissue_type="epithelioid carcinoma cell line"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_42"
                      /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                      Site_2: EcoRI; cDNA made by oligo-dT priming.
                      Directionally cloned into EcoRI/XhoI sites using the
                      following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                      for average insert size 1.8kb. Library constructed by Ling
                      Hong in the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies).
                      Note: this is a NIH_MGC Library. |"
BASE COUNT      143 a    248 c    245 g    124 t
ORIGIN

  Query Match             93.7%;  Score 47.8;  DB 12;  Length 760;
  Best Local Similarity   96.1%;  Pred. No. 1.9e-05;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||| |||| |||||||||||||||||||||||||||||||
Db        671 AGCAGAGGCAGCGGGTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 721


RESULT 5
BG829828
LOCUS       BG829828                932 bp    mRNA    linear   EST 22-MAY-2001
DEFINITION  602764119F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4899436 5',
            mRNA sequence.
ACCESSION   BG829828
VERSION     BG829828.1  GI:14177415
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 932)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1791  row: e  column: 05
            High quality sequence stop: 833.
FEATURES              Location/Qualifiers
     source           1. .932
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4899436"
                      /tissue_type="epithelioid carcinoma cell line"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_42"
                      /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                      Site_2: EcoRI; cDNA made by oligo-dT priming.
                      Directionally cloned into EcoRI/XhoI sites using the
                      following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                      for average insert size 1.8kb. Library constructed by Ling
                      Hong in the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies).
                      Note: this is a NIH_MGC Library. |"
BASE COUNT      162 a    296 c    296 g    177 t      1 others
ORIGIN

  Query Match             93.7%;  Score 47.8;  DB 12;  Length 932;
  Best Local Similarity   96.1%;  Pred. No. 2.1e-05;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||| |||| |||||||||||||||||||||||||||||||
Db        672 AGCAGAGGCAGCGGGTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 722


RESULT 6
BG745202
LOCUS       BG745202                974 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602723532F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4850143 5',
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            mRNA sequence.
ACCESSION   BG745202
VERSION     BG745202.1  GI:14055855
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 974)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1690  row: o  column: 08
            High quality sequence stop: 420.
FEATURES             Location/Qualifiers
     source          1. .974
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4850143"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      301 a    245 c    285 g    143 t
ORIGIN

  Query Match           93.7%;  Score 47.8;  DB 10;  Length 974;
  Best Local Similarity   96.1%;  Pred. No. 2.1e-05;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||| |||| ||||||||||||||||||||||||||||||||
Db         14 AGCAGAGGCAGCGGGTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 64


RESULT 7
BF568409
LOCUS       BF568409                1051 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602184408F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300633 5',
            mRNA sequence.
ACCESSION   BF568409
VERSION     BF568409.1  GI:11641789
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1051)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1159  row: o  column: 02
            High quality sequence stop: 769.
FEATURES             Location/Qualifiers
     source          1. .1051
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4300633"
                     /tissue_type="epithelioid carcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_42"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library. |"
BASE COUNT      229 a    313 c    346 g    161 t      2 others
ORIGIN

  Query Match           93.7%;  Score 47.8;  DB 10;  Length 1051;
  Best Local Similarity   96.1%;  Pred. No. 2.2e-05;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||| |||| ||||||||||||||||||||||||||||||||
Db        671 AGCAGAGGCAGCGGGTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 721


RESULT 8
BQ052282/c
LOCUS       BQ052282                1053 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6868457 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933511
            5', mRNA sequence.
ACCESSION   BQ052282
VERSION     BQ052282.1  GI:19811622
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1053)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2118  row: c  column: 16
            High quality sequence stop: 649.
FEATURES             Location/Qualifiers
     source          1. .1053
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5933511"
                     /tissue_type="natural killer cells, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_106"
                     /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
```

into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 216 a 328 c 297 g 212 t
ORIGIN

Query Match 93.7%; Score 47.8; DB 12; Length 1053;
Best Local Similarity 96.1%; Pred. No. 2.2e-05;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
||||||||||||||| |||| ||||||||||||||||||||||||||||||||||
Db 745 AGCAGAGGCAGCGGGTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 695

RESULT 9
BM917316
LOCUS BM917316 1102 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6606593 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5483819 5', mRNA sequence.
ACCESSION BM917316
VERSION BM917316.1 GI:19367695
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1102)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2012 row: b column: 12
High quality sequence stop: 507.
FEATURES Location/Qualifiers
source 1. .1102
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5483819"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 219 a 366 c 292 g 222 t 3 others
ORIGIN

Query Match 93.7%; Score 47.8; DB 12; Length 1102;
Best Local Similarity 96.1%; Pred. No. 2.2e-05;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
||||||||||||||| |||| ||||||||||||||||||||||||||||||||||
Db 172 AGCAGAGGCAGCGGGTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 222

RESULT 10
BF569011/c
LOCUS BF569011 1183 bp mRNA linear EST 12-DEC-2000
DEFINITION 602184353T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300500 3', mRNA sequence.
ACCESSION BF569011
VERSION BF569011.1 GI:11642391
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1183)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1159 row: i column: 13
High quality sequence stop: 716.
FEATURES Location/Qualifiers
source 1. .1183
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4300500"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_42"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"
BASE COUNT 308 a 357 c 348 g 170 t
ORIGIN

Query Match 69.0%; Score 35.2; DB 10; Length 1183;
Best Local Similarity 92.3%; Pred. No. 0.31;
Matches 48; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AGCAGAGGCAGC-GAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
||||||||||||| | ||| ||||||||||||||||||||||||||||||||||
Db 669 AGCAGAGGCAGCTGGTTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 618

RESULT 11
AV746487
LOCUS AV746487 472 bp mRNA linear EST 19-OCT-2000
DEFINITION AV746487 NPC Homo sapiens cDNA clone NPCAMA05 5', mRNA sequence.
ACCESSION AV746487
VERSION AV746487.1 GI:10904335
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 472)
AUTHORS Song,H., Peng,Y., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu ,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Zhang,Q.

```
            , Han,Z., Chen,Z., Hu,R. and Chen,J.
  TITLE     Homo sapiens NPC library cDNA clones
  JOURNAL   Unpublished
COMMENT     Contact: Qinghua Zhang
            Shanghai Institute of Endocrinology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64370045(ex.663332)
            Fax: 86-21-64743206
            Email: mbshi@ms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
FEATURES             Location/Qualifiers
     source          1. .472
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="NPCAMA05"
                     /tissue_type="pituitary"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="NPC"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT       63 a    137 c    150 g    112 t     10 others
ORIGIN

  Query Match             62.4%;  Score 31.8;  DB 9;  Length 472;
  Best Local Similarity   90.2%;  Pred. No. 2.8;
  Matches   46;  Conservative    0;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||| ||   |||||||||||||||| ||||||||||
Db         68 AGCAGAGGCAGCGAGTTGTGG---GCCTCTGCTGCCATGGCGTGTCCCTCT 115


RESULT 12
BX327945
LOCUS       BX327945                945 bp    mRNA    linear   EST 02-MAY-2003
DEFINITION  BX327945 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI063YP02 5-PRIME, mRNA sequence.
ACCESSION   BX327945
VERSION     BX327945.1  GI:30334709
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 945)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 266.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAG034ZF07_CS03222_2&cluster=266.f.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAG034ZF07_CS03222_2.
FEATURES             Location/Qualifiers
     source          1. .945
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI063YP02"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      194 a    295 c    280 g    168 t      8 others
ORIGIN

  Query Match             56.1%;  Score 28.6;  DB 13;  Length 945;
  Best Local Similarity   72.5%;  Pred. No. 41;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||| ||  |  |  ||| ||||||||| |||||||| || |  ||||| |
Db        872 AGCAAAGCAACGGGTTTGTGGAAAGCCTTTGCTGCCAGGGGGGTTCCCTTT 922


RESULT 13
AW176594
LOCUS       AW176594                150 bp    mRNA    linear   EST 16-NOV-1999
DEFINITION  RC5-CT0070-200899-001-H12 CT0070 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW176594
VERSION     AW176594.1  GI:6442631
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 150)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC5&t2=RC5-CT0070-
            200899-001-H12&t3=1999-08-20&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 150.
FEATURES             Location/Qualifiers
     source          1. .150
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="CT0070"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       26 a     55 c     41 g     28 t
ORIGIN

  Query Match             52.5%;  Score 26.8;  DB 9;  Length 150;
  Best Local Similarity   93.3%;  Pred. No. 79;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCT 30
              |||||||||||| |||| ||||||||||||
Db        121 AGCAGAGGCAGCGGGTTGTGGAAAGCCTCT 150


RESULT 14
AW062603
```

```
LOCUS       AW062603                175 bp    mRNA    linear   EST 06-OCT-1999
DEFINITION  RC0-CT0088-050899-001-B07 CT0088 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW062603
VERSION     AW062603.1  GI:6013988
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 175)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC0-CT0088-050
            899-001-B07&t3=1999-08-05&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 21
            High quality sequence stop: 175.
FEATURES             Location/Qualifiers
     source          1. .175
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="CT0088"
                     /note="Organ: colon; Vector: pUC18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       32 a     65 c     46 g     32 t
ORIGIN

  Query Match             52.5%;  Score 26.8;  DB 9;  Length 175;
  Best Local Similarity   93.3%;  Pred. No. 84;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCT 30
              ||||||||||||| |||| ||||||||||||
Db        146 AGCAGAGGCAGCGGGTTGTGGAAAGCCTCT 175


RESULT 15
BZ092262
LOCUS       BZ092262                689 bp    DNA     linear   GSS 10-OCT-2002
DEFINITION  CH230-232B6.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
            CH230-232B6, genomic survey sequence.
ACCESSION   BZ092262
VERSION     BZ092262.1  GI:23730376
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
            ,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
            Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 EcoRI segment
  JOURNAL   Unpublished
COMMENT     Other_GSSs: CH230-232B6.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 232  row: B  column: 6
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .689
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                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-232B6"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 1"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
BASE COUNT      211 a    159 c    128 g    191 t
ORIGIN

  Query Match             52.5%;  Score 26.8;  DB 28;  Length 689;
  Best Local Similarity   73.9%;  Pred. No. 1.4e+02;
  Matches   34;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTC 46
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Db        140 AGCAGAGGGACTCAGTAGGAGAAAGCATTTGCTGCCAGACTATGTC 185


Search completed: December 16, 2003, 19:04:16
Job time : 1356 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 15:51:34 ; Search time 147 Seconds
(without alignments)
936.540 Million cell updates/sec

Title: US-09-856-937A-1_COPY_580_630
Perfect score: 51
Sequence: 1 agcagaggcagcgagttggg.....ctgccatggtgtgtccctct 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	2224	16	AAQ89544	p75 Tumour Necrosi
2	51	100.0	2613	21	AAA49207	Human tumour necro
3	51	100.0	2613	24	ABZ35564	Human gene express
4	51	100.0	3683	24	ABZ34910	Human gene express
5	51	100.0	3683	24	ABQ74753	Human tumour necro
6	51	100.0	3683	24	ABK83997	Human cDNA differe
7	51	100.0	3683	24	ABL65877	Lung cancer relate
8	51	100.0	3683	24	ABK33465	Human TNF receptor
9	51	100.0	3683	24	ABK33466	Human TNF receptor
10	51	100.0	3683	24	ABK33467	Human TNF receptor
11	50.6	99.2	201	19	AAX12093	Human biallelic po
12	47.8	93.7	2339	12	AAQ10956	Encodes human 75kD
13	47.8	93.7	2339	20	AAZ09171	Human tumour necro
14	47.8	93.7	2339	22	AAH48860	Human TNFBP-associ
15	47.8	93.7	2393	12	AAQ10907	40kD TNF inhibitor
16	47.8	93.7	2394	22	AAC83951	Human 40 kDa TNF i
17	47.8	93.7	15602	24	ABQ74767	Human TNFR2 partia
18	42.4	83.1	51	22	AAL29880	Human SNP oligonuc
19	25.6	50.2	31	20	AAX06309	Human biallelic po
c 20	25.6	50.2	84	22	ABA50204	Human breast cell
c 21	25.6	50.2	84	22	ABA68144	Human foetal liver
c 22	25.6	50.2	84	22	ABA35162	Probe #13628 for g
c 23	25.6	50.2	84	22	AAK16524	Human brain expres
c 24	25.6	50.2	84	22	AAK42280	Human bone marrow
c 25	25.6	50.2	84	22	AAI23051	Probe #12984 for g
c 26	25.6	50.2	84	22	AAI48356	Probe #17042 used
c 27	25.6	50.2	84	22	AAI08708	Probe #8699 used t
c 28	25.6	50.2	84	23	ABS41888	Human liver single
c 29	25.6	50.2	84	24	ABS16331	Human genome-deriv
c 30	25.6	50.2	416	22	ABA45067	Human breast cell
c 31	25.6	50.2	416	22	ABA55546	Human foetal liver
c 32	25.6	50.2	416	22	ABA25250	Probe #3716 for ge
c 33	25.6	50.2	416	22	AAK03772	Human brain expres
c 34	25.6	50.2	416	22	AAK29240	Human bone marrow
c 35	25.6	50.2	416	22	AAI13833	Probe #3766 for ge
c 36	25.6	50.2	416	22	AAI35197	Probe #3883 used t
c 37	25.6	50.2	416	22	AAI03704	Probe #3695 used t
c 38	25.6	50.2	416	23	ABS28859	Human liver single
c 39	25.6	50.2	416	24	ABS03794	Human genome-deriv
40	25.6	50.2	464	22	ABA43185	Human breast cell
41	25.6	50.2	464	22	ABA53605	Human foetal liver
42	25.6	50.2	464	22	ABA23360	Probe #1826 for ge
43	25.6	50.2	464	22	AAK01871	Human brain expres
44	25.6	50.2	464	22	AAK27328	Human bone marrow
45	25.6	50.2	464	22	AAI11902	Probe #1835 for ge

ALIGNMENTS

RESULT 1
AAQ89544
ID AAQ89544 standard; DNA; 2224 BP.
XX
AC AAQ89544;
XX
DT 25-MAR-2003 (updated)
DT 31-OCT-1995 (first entry)
XX
DE p75 Tumour Necrosis Factor Receptor.
XX
KW Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
KW receptor; ss..
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 90..1475
FT /*tag= a
FT /product= p75 TNF receptor.
FT misc_difference 1137..1139
FT /*tag= b
FT /transl_except= GCA encodes Glycine.
FT misc_difference 1140..1142
FT /*tag= c
FT /transl_except= CCA encodes Alanine.
FT misc_difference 1146..1148
FT /*tag= d
FT /transl_except= GTG encodes Glutamic acid.
FT misc_difference 1149..1151
FT /*tag= e

```
FT                   /transl_except= GAG encodes Alanine.
FT   misc_difference 1152..1154
FT                   /*tag=  f
FT                   /transl_except= GCC encodes Arginine.
FT   misc_difference 1155..1157
FT                   /*tag=  g
FT                   /transl_except= AGT encodes Alanine.
FT   misc_difference 1158..1160
FT                   /*tag=  h
FT                   /transl_except= GGG encodes Serine.
FT   misc_difference 1161..1163
FT                   /*tag=  i
FT                   /transl_except= GCC encodes Threonine.
FT   misc_difference 1167..1169
FT                   /*tag=  j
FT                   /transl_except= GAG encodes Serine.
FT   misc_difference 1170..1172
FT                   /*tag=  k
FT                   /transl_except= GCC encodes Serine.
FT   misc_difference 1173..1175
FT                   /*tag=  l
FT                   /transl_except= CGG encodes Aspartic acid.
FT   misc_difference 1176..1178
FT                   /*tag=  m
FT                   /transl_except= GCC encodes Serine.
FT   misc_difference 1182..1184
FT                   /*tag=  n
FT                   /transl_except= ACC encodes Proline.
FT   misc_difference 1188..1190
FT                   /*tag=  o
FT                   /transl_except= AGC encodes Glycine.
FT   misc_difference 1191..1193
FT                   /*tag=  p
FT                   /transl_except= TCA encodes Histidine.
FT   misc_difference 1194..1196
FT                   /*tag=  q
FT                   /transl_except= GAT encodes Glycine.
FT   misc_difference 1197..1199
FT                   /*tag=  r
FT                   /transl_except= TCT encodes Threonine.
FT   misc_difference 2000..2002
FT                   /*tag=  s
FT                   /transl_except= TCC encodes Glutamine.
FT   misc_difference 2003..2005
FT                   /*tag=  t
FT                   /transl_except= CCT encodes Alanine.
FT   misc_difference 2006..2008
FT                   /*tag=  u
FT                   /transl_except= GGT encodes Proline.
FT   misc_difference 2012..2014
FT                   /*tag=  v
FT                   /transl_except= CAT encodes Valine.
FT   misc_difference 2015..2016
FT                   /*tag=  w
FT                   /transl_except= GGG encodes Glutamic acid.
FT   misc_difference 2017..2018
FT                   /*tag=  x
FT                   /transl_except= ACC encodes Alanine.
FT   misc_difference 2019..2021
FT                   /*tag=  y
FT                   /transl_except= CAG encodes Serine.
XX
PN   EP648783-A1.
XX
PD   19-APR-1995.
XX
PF   11-OCT-1994;   94EP-0116015.
XX
PR   12-OCT-1993;   93IL-0107267.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
PA   (WALL/) WALLACH D.
XX
PI   Beletsky I,  Bigda J,  Mett I,  Wallach D;
XX
DR   WPI; 1995-148673/20.
DR   P-PSDB; AAR72504.
XX
PT   Tumour necrosis factor (TNF) receptor ligand - used to increase
PT   inhibitory effect of a soluble TNF receptor
XX
PS   Disclosure; Figure 2; 18pp; English.
XX
CC   A ligand to a member of the tumour necrosis factor (TNF)/nerve
CC   growth factor (NGF) receptor family which binds either to the region
CC   of the 4th-Cys rich domain of the receptor, or to the region between
CC   it and the cell membrane may be used in the production of a
CC   pharmaceutical composition for increasing the inhibitory effect of a
CC   soluble receptor of the TNF/NGF receptor family.  This sequence
CC   encodes the p75 TNF receptor.  N in the sequence represents an
CC   unidentified nucleotide (poor reproduction in specification).
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2224 BP; 432 A; 697 C; 688 G; 400 T; 7 other;

  Query Match             100.0%;  Score 51;  DB 16;  Length 2224;
  Best Local Similarity   100.0%;  Pred. No. 3e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 2
AAA49207
ID   AAA49207 standard; DNA; 2613 BP.
XX
AC   AAA49207;
XX
DT   22-NOV-2000  (first entry)
XX
DE   Human tumour necrosis factor alpha receptor 2 gene exon 10.
XX
KW   Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;
KW   osteoporosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..2613
FT                   /*tag=  a
FT                   /product= "TNFR2"
FT                   /partial
FT   allele          replace (593,A), (598,G), (620,T)
FT                   /*tag=  b
FT                   /label= allele_1
FT   allele          replace (593,A), (598,T), (620,T)
FT                   /*tag=  c
FT                   /label= allele_2
FT   allele          replace (593,G), (598,T), (620,C)
FT                   /*tag=  d
FT                   /label= allele_3
FT   allele          replace (593,G), (598,T), (620,T)
FT                   /*tag=  e
FT                   /label= allele_4
FT   allele          replace (593,A), (598,T), (620,C)
FT                   /*tag=  f
FT                   /label= allele_5
XX
PN   WO200032826-A1.
XX
PD   08-JUN-2000.
XX
PF   30-NOV-1999;   99WO-US28403.
XX
```

PR 30-NOV-1998; 98US-0110268.
XX
PA (UYDR-) UNIV DREXEL.
XX
PI Spotila LD;
XX
DR WPI; 2000-412362/35.
XX
PT Identifying individuals at risk of developing osteoporosis comprises
PT assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene
PT in a DNA sample from an individual -
XX
PS Claim 2; Page 17-18; 21pp; English.
XX
CC The present sequence comprises exon 10 of the human tumour necrosis
CC factor alpha receptor 2 (THFR2) gene. The sequence contains three
CC polymorphic sites. By determining the genotype of an individual it is
CC possible to identify those at risk of osteoporosis, which is
CC characterised by low bone density and fragile bones, later in life. Those
CC at greatest risk are those who possess allele 1, which is the rarest
CC allele. This is particularly useful as many cases of osteoporosis go
CC undetected at present.
XX
SQ Sequence 2613 BP; 553 A; 750 C; 742 G; 568 T; 0 other;

Query Match 100.0%; Score 51; DB 21; Length 2613;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 580 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 630

RESULT 3
ABZ35564
ID ABZ35564 standard; cDNA; 2613 BP.
XX
AC ABZ35564;
XX
DT 05-FEB-2003 (first entry)
XX
DE Human gene expression profile polynucleotide SEQ ID NO 675.
XX
KW Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW gene expression; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200274979-A2.
XX
PD 26-SEP-2002.
XX
PF 20-MAR-2002; 2002WO-US08456.
XX
PR 20-MAR-2001; 2001US-276947P.
XX
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Wan J, Wang Y;
XX
DR WPI; 2002-740862/80.
XX
PT New gene expression profile generated from primary, endothelial,
PT epithelial, and muscle cell types, useful for identifying disease
PT pathologies involving alterations of gene expression, e.g. cancer -
XX
PS Example 3; Page 798-799; 850pp; English.
XX
CC The invention relates to a gene expression profile comprising one or more
CC genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
CC is a coronary artery endothelium, umbilical artery or vein endothelium,
CC aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC endothelium, myometrium microvascular endothelium, keratinocyte
CC epithelium, bronchial epithelium, mammary epithelium, prostate
CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,
CC small airway epithelium, renal epithelium, umbilical artery smooth
CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
CC osteoblasts or prostate stromal cell. The gene expression profile is used
CC for determining the level of RNA expression for a sample, determining the
CC phenotype of a cell and distinguishing cell types. The gene or a protein
CC expression profile is useful in identifying disease pathologies
CC involving alterations of gene expression. The assessment of expression
CC profiles may provide meaningful information with respect to tumour type
CC and stage, treatment methods, and prognosis. The gene or protein
CC expression profile may also be used for creating microarrays. The
CC microarray is useful for genetic and physical mapping of genomes, DNA
CC sequencing, genetic or medical diagnosis, genotyping of organisms,
CC confirming cell or tissue identifications and in identifying promising
CC antibiotics, antiviral or antifungal agents.
XX
SQ Sequence 2613 BP; 553 A; 750 C; 742 G; 568 T; 0 other;

Query Match 100.0%; Score 51; DB 24; Length 2613;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 580 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 630

RESULT 4
ABZ34910
ID ABZ34910 standard; cDNA; 3683 BP.
XX
AC ABZ34910;
XX
DT 05-FEB-2003 (first entry)
XX
DE Human gene expression profile polynucleotide SEQ ID NO 22.
XX
KW Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW gene expression; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200274979-A2.
XX
PD 26-SEP-2002.
XX
PF 20-MAR-2002; 2002WO-US08456.
XX
PR 20-MAR-2001; 2001US-276947P.
XX
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Wan J, Wang Y;
XX
DR WPI; 2002-740862/80.
XX
PT New gene expression profile generated from primary, endothelial,
PT epithelial, and muscle cell types, useful for identifying disease
PT pathologies involving alterations of gene expression, e.g. cancer -
XX
PS Claim 1; Page 235-236; 850pp; English.
XX
CC The invention relates to a gene expression profile comprising one or more
CC genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type

```
CC   is a coronary artery endothelium, umbilical artery or vein endothelium,
CC   aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC   endothelium, myometrium microvascular endothelium, keratinocyte
CC   epithelium, bronchial epithelium, mammary epithelium, prostate
CC   epithelium, renal cortical epithelium, renal proximal tubule epithelium,
CC   small airway epithelium, renal epithelium, umbilical artery smooth
CC   muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
CC   dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
CC   aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
CC   bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
CC   osteoblasts or prostate stromal cell. The gene expression profile is used
CC   for determining the level of RNA expression for a sample, determining the
CC   phenotype of a cell and distinguishing cell types. The gene or a protein
CC   expression profile is useful in identifying disease pathologies
CC   involving alterations of gene expression. The assessment of expression
CC   profiles may provide meaningful information with respect to tumour type
CC   and stage, treatment methods, and prognosis. The gene or protein
CC   expression profile may also be used for creating microarrays. The
CC   microarray is useful for genetic and physical mapping of genomes, DNA
CC   sequencing, genetic or medical diagnosis, genotyping of organisms,
CC   confirming cell or tissue identifications and in identifying promising
CC   antibiotics, antiviral or antifungal agents.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 5
ABQ74753
ID   ABQ74753 standard; cDNA; 3683 BP.
XX
AC   ABQ74753;
XX
DT   24-OCT-2002  (first entry)
XX
DE   Human tumour necrosis factor receptor 2 encoding cDNA SEQ ID NO:3.
XX
KW   Tumour necrosis factor receptor 2; TNFR2; antisense oligonucleotide;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "tumour necrosis factor receptor 2"
XX
PN   US6410324-B1.
XX
PD   25-JUN-2002.
XX
PF   27-APR-2001; 2001US-0844634.
XX
PR   27-APR-2001; 2001US-0844634.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Watt AT;
XX
DR   WPI; 2002-606814/65.
DR   P-PSDB; ABP52451.
XX
PT   New compounds antisense to nucleic acid encoding human or mouse tumor
PT   necrosis factor receptor 2 are useful to treat disease associated with
PT   mouse tumor necrosis factor receptor 2 expression  -
XX
PS   Claim 1; Column 53-58; 69pp; English.
XX
CC   The present invention describes compounds of 8-30 nucleobases antisense
CC   to a nucleic acid encoding human or mouse tumour necrosis factor
CC   receptor 2 (TNFR2). Also described is a method for inhibiting expression
CC   of human or mouse TNFR2 comprising contacting cells or tissues in vitro
CC   with one of the claimed compounds. The antisense compounds are used to
CC   treat a disease or condition associated with expression of TNFR2. The
CC   present sequence encodes human TNFR2, which is used in an example from
CC   the present invention.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 6
ABK83997
ID   ABK83997 standard; cDNA; 3683 BP.
XX
AC   ABK83997;
XX
DT   14-AUG-2002  (first entry)
XX
DE   Human cDNA differentially expressed in granulocytic cells #568.
XX
KW   Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW   viral infection; parasitic infection; protozoal infection;
KW   fungal infection; sterile inflammatory disease; psoriasis;
KW   rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW   cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW   adult respiratory distress syndrome; inflammatory bowel disease;
KW   Crohn's disease; ulcerative colitis; periodontal disease;
KW   granulocyte activation; chronic inflammation; allergy.
XX
OS   Homo sapiens.
XX
PN   WO200228999-A2.
XX
PD   11-APR-2002.
XX
PF   03-OCT-2001; 2001WO-US30821.
XX
PR   03-OCT-2000; 2000US-237189P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Beazer-Barclay Y,  Weissman SM,  Yamaga S,  Vockley J;
XX
DR   WPI; 2002-435328/46.
XX
PT   Detecting granulocyte activation by detecting differential expression
PT   of genes associated with granulocyte activation, which serves as
PT   diagnostic markers that is useful for monitoring disease states and
PT   drug toxicity  -
XX
PS   Claim 1; SEQ ID No 568; 114pp; English.
XX
CC   The invention relates to detecting (M1) granulocyte (GC) activation
CC   (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC   DNA chip analysis as given in the specification, and comparing
CC   the expression level to an expression level in an unactivated
CC   GC, where differential expression of Gs is indicative of GCA.
CC   Also included are modulating (M2) GA by contacting GC with an agent
CC   that alters the expression of at least one gene in Gs; (2) screening (M3)
CC   for an agent capable of modulating GCA or an inflammation (especially
CC   chronic) in a tissue, an allergic response in a subject, exposure of a
```

CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

Query Match 100.0%; Score 51; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700

RESULT 7
ABL65877
ID ABL65877 standard; DNA; 3683 BP.
XX
AC ABL65877;
XX
DT 15-MAY-2002 (first entry)
XX
DE Lung cancer related gene sequence SEQ ID NO:4214.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set
XX
PS Claim 1; SEQ ID 4214; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

Query Match 100.0%; Score 51; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700

```
RESULT 8
ABK33465
ID   ABK33465 standard; DNA; 3683 BP.
XX
AC   ABK33465;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human TNF receptor II gene.
XX
KW   Human; anti-tumour necrosis factor receptor II; TNF receptor II;
KW   chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW   inflammatory disorder; chronic disease; receptor; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "TNF receptor II"
FT   sig_peptide     90..155
FT                   /*tag=  b
FT   mat_peptide     156..1472
FT                   /*tag=  c
XX
PN   EP1172444-A1.
XX
PD   16-JAN-2002.
XX
PF   10-JUL-2000; 2000EP-0114786.
XX
PR   10-JUL-2000; 2000EP-0114786.
XX
PA   (CONA-) CONARIS RES INST GMBH.
XX
PI   Schreiber S,  Hampe J,  Mascheretti S;
XX
DR   WPI; 2002-156651/21.
DR   P-PSDB; AAU75172.
XX
PT   Detecting non-responders to anti-human necrosis factor therapy,
PT   comprises testing an individual for homozygosity for a single
PT   nucleotide polymorphism in the gene coding for the tumour necrosis
PT   factor receptor II  -
XX
PS   Disclosure; Page 23-27; 45pp; English.
XX
CC   The present invention relates to a method for detecting non-responders
CC   to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC   an individual for homozygosity for at least one single nucleotide
CC   polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC   located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC   A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC   Met196Arg respectively, are also described. The method of the invention
CC   is useful for detecting non-responders to anti-TNF therapy such as
CC   infliximab therapy, or therapy of Crohn's disease. The genes containing
CC   the 2 novel polymorphisms are useful for diagnostic purposes in
CC   inflammatory, malignant or other chronic diseases. The present sequence
CC   encodes for human TNF receptor II.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 9
ABK33466
ID   ABK33466 standard; DNA; 3683 BP.
XX
AC   ABK33466;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human TNF receptor II gene with SNP in exon 2.
XX
KW   Human; anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
KW   chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW   inflammatory disorder; chronic disease; receptor; gene;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "TNF receptor II variant #1"
FT   sig_peptide     90..155
FT                   /*tag=  b
FT   mat_peptide     156..1472
FT                   /*tag=  c
FT   variation       replace (257, A)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   EP1172444-A1.
XX
PD   16-JAN-2002.
XX
PF   10-JUL-2000; 2000EP-0114786.
XX
PR   10-JUL-2000; 2000EP-0114786.
XX
PA   (CONA-) CONARIS RES INST GMBH.
XX
PI   Schreiber S,  Hampe J,  Mascheretti S;
XX
DR   WPI; 2002-156651/21.
DR   P-PSDB; AAU75173.
XX
PT   Detecting non-responders to anti-human necrosis factor therapy,
PT   comprises testing an individual for homozygosity for a single
PT   nucleotide polymorphism in the gene coding for the tumour necrosis
PT   factor receptor II  -
XX
PS   Claim 15; Page 29-33; 45pp; English.
XX
CC   The present invention relates to a method for detecting non-responders
CC   to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC   an individual for homozygosity for at least one single nucleotide
CC   polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC   located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC   A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC   Met196Arg respectively, are also described. The method of the invention
CC   is useful for detecting non-responders to anti-TNF therapy such as
CC   infliximab therapy, or therapy of Crohn's disease. The genes containing
CC   the 2 novel polymorphisms are useful for diagnostic purposes in
CC   inflammatory, malignant or other chronic diseases. The present sequence
CC   represents the human TNF receptor II gene containing the SNP in exon 2.
XX
SQ   Sequence 3683 BP; 780 A; 1098 C; 1087 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700
```

```
RESULT 10
ABK33467
ID   ABK33467 standard; DNA; 3683 BP.
XX
AC   ABK33467;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human TNF receptor II gene with SNP in exon 6.
XX
KW   Human; anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
KW   chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW   inflammatory disorder; chronic disease; receptor; gene;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "TNF receptor II variant #2"
FT   sig_peptide     90..155
FT                   /*tag=  b
FT   mat_peptide     156..1472
FT                   /*tag=  c
FT   variation       replace (676, T)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   EP1172444-A1.
XX
PD   16-JAN-2002.
XX
PF   10-JUL-2000; 2000EP-0114786.
XX
PR   10-JUL-2000; 2000EP-0114786.
XX
PA   (CONA-) CONARIS RES INST GMBH.
XX
PI   Schreiber S,  Hampe J,  Mascheretti S;
XX
DR   WPI; 2002-156651/21.
DR   P-PSDB; AAU75174.
XX
PT   Detecting non-responders to anti-human necrosis factor therapy,
PT   comprises testing an individual for homozygosity for a single
PT   nucleotide polymorphism in the gene coding for the tumour necrosis
PT   factor receptor II  -
XX
PS   Claim 16; Page 35-39; 45pp; English.
XX
CC   The present invention relates to a method for detecting non-responders
CC   to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC   an individual for homozygosity for at least one single nucleotide
CC   polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC   located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC   A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC   Met196Arg respectively, are also described. The method of the invention
CC   is useful for detecting non-responders to anti-TNF therapy such as
CC   infliximab therapy, or therapy of Crohn's disease. The genes containing
CC   the 2 novel polymorphisms are useful for diagnostic purposes in
CC   inflammatory, malignant or other chronic diseases. The present sequence
CC   represents the human TNF receptor II gene containing the SNP in exon 6.
XX
SQ   Sequence 3683 BP; 780 A; 1098 C; 1088 G; 717 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-09;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 11
AAX12093
ID   AAX12093 standard; DNA; 201 BP.
XX
AC   AAX12093;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Human biallelic polymorphic DNA fragment M32315b.
XX
KW   Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW   detection; phenotypic typing; characteristic; infection; hereditary;
KW   autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW   treatment; marker; ss.
XX
OS   Homo sapiens.
XX
PN   WO9820165-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US20313.
XX
PR   06-NOV-1996;   96US-0030455.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Hudson T,  Lander ES,  Wang D;
XX
DR   WPI; 1998-286974/25.
XX
PT   New isolated nucleic acid segments from the human genome - used for
PT   determining polymorphic forms for use in e.g. forensics, paternity
PT   testing or phenotypic typing for disease
XX
PS   Claim 1; Page 219; 310pp; English.
XX
CC   AAX10269-X12937 are human DNA fragments which contain biallelic
CC   polymorphic markers which have been isolated using the primers
CC   represented in AAX09121-X10268. The base occupying the polymorphic site
CC   is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC   can be used in methods for determining polymorphic forms in an individual
CC   for use in e.g. forensics, paternity testing or for phenotypic typing for
CC   diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
CC   syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC   familial hypercholesterolemia, polycystic kidney disease, hereditary
CC   spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC   haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC   syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC   autoimmune diseases, inflammation, cancer, diseases of the nervous
CC   system, infection by pathogenic microorganisms, and characteristics such
CC   as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC   endurance, fertility, and susceptibility or receptivity to particular
CC   drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC   segments can also be used to produce medicaments for the treatment or
CC   prophylaxis of such diseases.
XX
SQ   Sequence 201 BP; 32 A; 65 C; 62 G; 41 T; 1 other;

  Query Match             99.2%;  Score 50.6;  DB 19;  Length 201;
  Best Local Similarity   98.0%;  Pred. No. 2.8e-09;
  Matches   50;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db         90 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGYGTGTCCCTCT 140


RESULT 12
AAQ10956
```

```
ID   AAQ10956 standard; DNA; 2339 BP.
XX
AC   AAQ10956;
XX
DT   09-JAN-2003  (updated)
DT   24-MAY-1991  (first entry)
XX
DE   Encodes human 75kD TNF-binding protein.
XX
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1179
FT                   /*tag=  a
FT                   /product= 75kD TNF-BP
XX
PN   EP417563-A.
XX
PD   20-MAR-1991.
XX
PF   31-AUG-1990;   90EP-0116707.
XX
PR   20-APR-1990;   90CH-0001347.
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
XX
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Lotscher H;
PI   Schlaeger EJ;
XX
DR   WPI; 1991-081851/12.
DR   P-PSDB; AAR11605.
XX
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
XX
PS   Claim 4; Fig 1; 26pp; German.
XX
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. Repeated sequencing showed a discrepancy
CC   at position 7 such that the third codon encodes either Thr or Ser.
CC   DNA constructs comprising the TNF-BP coding sequence may also
CC   contain a fragment encoding a human Ig domain. Recombinant
CC   constructs are used to transform cells to confer improved TNF-
CC   binding properties.
CC   See also AAQ10955.
CC   (Updated on 09-JAN-2003 to add missing OS field.)
XX
SQ   Sequence 2339 BP; 494 A; 720 C; 685 G; 439 T; 1 other;

  Query Match             93.7%;  Score 47.8;  DB 12;  Length 2339;
  Best Local Similarity   96.1%;  Pred. No. 4.7e-08;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||| |||||||||||||||||| ||||||||||
Db       1353 AGCAGAGGCAGCGAGTTGTGGAAAGCCTCTGCTGCCATGGCGTGTCCCTCT 1403


RESULT 13
AAZ09171
ID   AAZ09171 standard; cDNA; 2339 BP.
XX
AC   AAZ09171;
XX
DT   20-MAR-2003  (updated)
DT   18-OCT-1999  (first entry)
XX
DE   Human tumour necrosis factor binding protein cDNA fragment.
XX
KW   Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KW   anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW   autoimmune glomerulonephritis; cerebral malaria; immune response;
KW   antagonist; diagnosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1179
FT                   /*tag=  a
FT                   /product= "TNF binding protein"
FT                   /note= "Partial sequence, no start codon given"
XX
PN   EP939121-A2.
XX
PD   01-SEP-1999.
XX
PF   31-AUG-1990;   99EP-0100703.
XX
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
PR   20-APR-1990;   90CH-0001347.
PR   31-AUG-1990;   90EP-0116707.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 1999-480840/41.
DR   P-PSDB; AAY30935.
XX
PT   New insoluble proteins, and fragments, that bind to tumor necrosis
PT   factor, used to treat e.g. septic shock or cerebral malaria
XX
PS   Claim 4a; Fig 4; 25pp; German.
XX
CC   This invention describes novel homogeneous insoluble proteins (I),
CC   their (in)soluble fragments (Ia) and their salts that can bind tumour
CC   necrosis factor (TNF). The products of the invention have
CC   anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC   to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC   glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC   (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC   diagnostic determination of TNF in body fluids. Antibodies raised against
CC   (I) are used for affinity purification of (I). This sequence encodes
CC   a tumour necrosis factor binding protein fragment described in the method
CC   of the invention.
CC   (Updated on 20-MAR-2003 to correct PF field.)
CC   (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ   Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;

  Query Match             93.7%;  Score 47.8;  DB 20;  Length 2339;
  Best Local Similarity   96.1%;  Pred. No. 4.7e-08;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||| |||||||||||||||||| ||||||||||
Db       1353 AGCAGAGGCAGCGAGTTGTGGAAAGCCTCTGCTGCCATGGCGTGTCCCTCT 1403


RESULT 14
AAH48860
ID   AAH48860 standard; DNA; 2339 BP.
XX
AC   AAH48860;
```

```
XX
DT   12-NOV-2001  (first entry)
XX
DE   Human TNFBP-associated DNA #2.
XX
KW   TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW   insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW   antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
KW   autoimmune glomerulonephritis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1179
FT                   /*tag=  a
FT                   /product= "TNFBP-associated protein"
XX
PN   EP1132471-A2.
XX
PD   12-SEP-2001.
XX
PF   31-AUG-1990; 2001EP-0108117.
XX
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
PR   20-APR-1990;   90CH-0001347.
PR   31-AUG-1990;   90EP-0116707.
PR   31-AUG-1990;   99EP-0100703.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 2001-559312/63.
DR   P-PSDB; AAB86818.
XX
PT   New homogeneous, insoluble proteins that bind tumor necrosis factor
PT   (TNF), useful for treating TNF-mediated disorders, e.g. inflammation  -
XX
PS   Claim 4a; Fig 4; 26pp; German.
XX
CC   This invention describes novel insoluble proteins (I), also their
CC   (in)soluble fragments and pharmaceutically acceptable salts, able to bind
CC   tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC   invention have antiinflammatory, immunosuppressive, antibacterial,
CC   antiprotozoal activity. (I), and related recombinant proteins, are used
CC   to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC   sepsis; development of autoimmune glomerulonephritis and cerebral
CC   malaria. Also (I), or antibodies specific for them, are used for
CC   diagnostic determination of TNF in body fluids, for affinity purification
CC   of TNF and for identifying (ant)agonists of TNF. This sequence encodes a
CC   human TNF binding protein described in the method of the invention.
XX
SQ   Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;

  Query Match             93.7%;  Score 47.8;  DB 22;  Length 2339;
  Best Local Similarity   96.1%;  Pred. No. 4.7e-08;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||| |||||||||||||||||| ||||||||||
Db       1353 AGCAGAGGCAGCGAGTTGTGGAAAGCCTCTGCTGCCATGGCGTGTCCCTCT 1403


RESULT 15
AAQ10907
ID   AAQ10907 standard; cDNA; 2393 BP.
XX
AC   AAQ10907;
XX
DT   25-MAR-2003  (updated)
DT   13-MAY-1991  (first entry)
XX
DE   40kD TNF inhibitor precursor gene in c40DK#6.
XX
KW   Tumour necrosis factor; inhibitor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             93..1478
FT                   /*tag=  a
XX
PN   AU9058976-A.
XX
PD   24-JAN-1991.
XX
PF   16-JUL-1990;   90AU-0058976.
XX
PR   07-FEB-1990;   90US-0479661.
PR   18-JUL-1989;   89US-0381080.
PR   11-DEC-1989;   89US-0450329.
XX
PA   (SYND ) SYNERGEN INC.
XX
DR   WPI; 1991-073847/11.
DR   P-PSDB; AAR11001.
XX
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
XX
PS   Disclosure; Fig 39; 142pp; English.
XX
CC   The sequence encodes the entire 40 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA.   The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also AAQ10878, AAQ10884 and AAQ10883.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 2393 BP; 484 A; 743 C; 738 G; 428 T; 0 other;

  Query Match             93.7%;  Score 47.8;  DB 12;  Length 2393;
  Best Local Similarity   96.1%;  Pred. No. 4.7e-08;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||| |||| ||||||||||||||||||||||||||||||||
Db       1652 AGCAGAGGCAGCGGGTTGTGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1702


Search completed: December 16, 2003, 18:21:06
Job time : 148 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 18:41:41 ; Search time 148 Seconds
(without alignments)
1145.294 Million cell updates/sec

Title: US-09-856-937A-1_COPY_580_630
Perfect score: 51
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	51	100.0	2224	10	US-09-800-908-2	Sequence 2, Appli
	3	51	100.0	2613	13	US-10-101-510-675	Sequence 675, App
	4	51	100.0	3683	10	US-09-954-456-1187	Sequence 1187, Ap
	5	51	100.0	3683	11	US-09-902-176A-49	Sequence 49, Appl
	6	51	100.0	3683	11	US-09-902-176A-51	Sequence 51, Appl
	7	51	100.0	3683	11	US-09-902-176A-53	Sequence 53, Appl
	8	51	100.0	3683	13	US-10-101-510-22	Sequence 22, Appl
	9	47.8	93.7	3492	15	US-10-207-655-191	Sequence 191, App
c	10	25.6	50.2	84	9	US-09-864-761-20482	Sequence 20482, A
c	11	25.6	50.2	416	9	US-09-864-761-3716	Sequence 3716, Ap
	12	25.6	50.2	464	9	US-09-864-761-1826	Sequence 1826, Ap
c	13	25.6	50.2	1082	13	US-10-027-632-86806	Sequence 86806, A
c	14	25.6	50.2	1082	14	US-10-027-632-86806	Sequence 86806, A
	15	24.8	48.6	426	9	US-09-864-761-23584	Sequence 23584, A
c	16	24.8	48.6	458	9	US-09-864-761-219	Sequence 219, App
	17	24.8	48.6	571	9	US-09-864-761-6851	Sequence 6851, Ap
c	18	24.8	48.6	1168	13	US-10-007-926A-349	Sequence 349, App
c	19	24.8	48.6	1683	13	US-10-115-831-22	Sequence 22, Appl
	20	24.4	47.8	26	11	US-09-902-176A-41	Sequence 41, Appl
c	21	24.4	47.8	2196	15	US-10-156-761-2559	Sequence 2559, Ap
	22	24.4	47.8	9700	10	US-09-953-342-1	Sequence 1, Appli
	23	24.4	47.8	9025608	15	US-10-156-761-1	Sequence 1, Appli
	24	23.8	46.7	425	11	US-09-918-995-34929	Sequence 34929, A
	25	23.8	46.7	598	13	US-10-027-632-32694	Sequence 32694, A
	26	23.8	46.7	598	14	US-10-027-632-32694	Sequence 32694, A
	27	23.6	46.3	2216	9	US-09-822-849A-516	Sequence 516, App
	28	23.4	45.9	1014	15	US-10-083-168-97	Sequence 97, Appl
c	29	23.2	45.5	209	10	US-09-878-178-1315	Sequence 1315, Ap
c	30	23.2	45.5	209	14	US-10-046-935-1315	Sequence 1315, Ap
c	31	23.2	45.5	209	15	US-10-146-502-1315	Sequence 1315, Ap
	32	23.2	45.5	318	9	US-09-864-761-29824	Sequence 29824, A
c	33	23.2	45.5	480	11	US-09-918-995-1297	Sequence 1297, Ap
	34	23.2	45.5	508	9	US-09-864-761-13255	Sequence 13255, A
	35	23.2	45.5	600	13	US-10-257-826A-257	Sequence 257, App
	36	23.2	45.5	674	13	US-10-257-826A-258	Sequence 258, App
c	37	23.2	45.5	1102	9	US-09-925-301-477	Sequence 477, App
c	38	23.2	45.5	1102	15	US-10-106-698-342	Sequence 342, App
c	39	23.2	45.5	1328	15	US-10-166-218-9	Sequence 9, Appli
c	40	23.2	45.5	1803	13	US-10-190-942-1	Sequence 1, Appli
	41	23.2	45.5	99916	10	US-09-816-095-3	Sequence 3, Appli
	42	23	45.1	7615	11	US-09-898-616A-9	Sequence 9, Appli
	43	23	45.1	7615	13	US-10-187-498A-9	Sequence 9, Appli
c	44	22.8	44.7	355	10	US-09-960-352-7539	Sequence 7539, Ap
	45	22.8	44.7	5340	9	US-09-817-360-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-09-800-909-1
; Sequence 1, Application US/09800909
; Patent No. US20010019833A1
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BIGDA, Jacek
;    APPLICANT:  BELETSKY, Igor
;    APPLICANT:  METT, Igor
;    APPLICANT:  ENGELMANN, Hartmut
;    TITLE OF INVENTION:  TNF INHIBITORS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/800,909
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/476,862
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 94039
;      FILING DATE:  06-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 91229
;      FILING DATE:  06-AUG-1989
;    PRIOR APPLICATION DATA:
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;       APPLICATION NUMBER:  IL 90339
;       FILING DATE:  18-MAY-1989
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BROWDY, Roger L.
;       REGISTRATION NUMBER:  25,618
;       REFERENCE/DOCKET NUMBER:  WALLACH=12A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2224 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  90..1472
US-09-800-909-1

  Query Match             100.0%;  Score 51;  DB 9;  Length 2224;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-10;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 2
US-09-800-908-2
; Sequence 2, Application US/09800908
; Patent No. US20020111462A1
;   GENERAL INFORMATION:
;       APPLICANT: WALLACH, David
;                  BIGDA, Jacek
;                  BELETSKY, Igor
;                  METT, Igor
;       TITLE OF INVENTION: TNF LIGANDS
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/800,908
;            FILING DATE: 08-Mar-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/477,347
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: IL 106271
;            FILING DATE: 08-JUL-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Townsend, G. Kevin
;            REGISTRATION NUMBER: 34,033
;            REFERENCE/DOCKET NUMBER: WALLACH=10
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;            TELEX: 248633
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2224 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  90..1472
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-800-908-2

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  Best Local Similarity   100.0%;  Pred. No. 8.4e-10;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-10-101-510-675
; Sequence 675, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
;  APPLICANT: WAN, JACKSON
;  APPLICANT:  WANG, YIXIN
;  TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
;  FILE REFERENCE: 15117.0012
;  CURRENT APPLICATION NUMBER: US/10/101,510
;  CURRENT FILING DATE:  2002-03-20
;  PRIOR APPLICATION NUMBER: 60/276,947
;  PRIOR FILING DATE: 2001-03-20
;  NUMBER OF SEQ ID NOS: 805
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 675
;   LENGTH: 2613
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-101-510-675

  Query Match             100.0%;  Score 51;  DB 13;  Length 2613;
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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db        580 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 630


RESULT 4
US-09-954-456-1187
; Sequence 1187, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
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;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1187
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-1187

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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 5
US-09-902-176A-49
; Sequence 49, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (90)..(1475)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (156)
US-09-902-176A-49

  Query Match           100.0%;  Score 51;  DB 11;  Length 3683;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-10;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 6
US-09-902-176A-51
; Sequence 51, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (90)..(1475)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (156)
US-09-902-176A-51

  Query Match           100.0%;  Score 51;  DB 11;  Length 3683;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-10;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 7
US-09-902-176A-53
; Sequence 53, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (90)..(1475)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (156)
US-09-902-176A-53

  Query Match           100.0%;  Score 51;  DB 11;  Length 3683;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-10;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 8
US-10-101-510-22
; Sequence 22, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
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;  APPLICANT: WAN, JACKSON
;  APPLICANT:  WANG, YIXIN
;  TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
;  FILE REFERENCE: 15117.0012
;  CURRENT APPLICATION NUMBER: US/10/101,510
;  CURRENT FILING DATE:  2002-03-20
;  PRIOR APPLICATION NUMBER: 60/276,947
;  PRIOR FILING DATE: 2001-03-20
;  NUMBER OF SEQ ID NOS: 805
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-101-510-22

  Query Match             100.0%;  Score 51;  DB 13;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-10;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 9
US-10-207-655-191
; Sequence 191, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 191
;   LENGTH: 3492
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-207-655-191

  Query Match             93.7%;  Score 47.8;  DB 15;  Length 3492;
  Best Local Similarity   96.1%;  Pred. No. 1.4e-08;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db       1453 AGCAGAGGCAGCGAGTTGTGGAAAGCCTCTGCTGCCATGGCGTGTCCCTCT 1503


RESULT 10
US-09-864-761-20482/c
; Sequence 20482, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20482
;   LENGTH: 84
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000010.2
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL =   1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;   OTHER INFORMATION: NT HIT: Y09912.1, EVALUE 5.80e-01
;   OTHER INFORMATION: EST_HUMAN HIT: BE047094.1, EVALUE 3.00e-06
US-09-864-761-20482

  Query Match             50.2%;  Score 25.6;  DB 9;  Length 84;
  Best Local Similarity   77.5%;  Pred. No. 3.3;
  Matches   31;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          5 GAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTG 44
              |||  | || |  |||||||||| |||| ||| |||||||
Db         43 GAGCAAACGTGAAGGGGAAAGCCACTGCAGCCGTGGTGTG 4


RESULT 11
US-09-864-761-3716/c
; Sequence 3716, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
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;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3716
;   LENGTH: 416
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000010.2
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL =   1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
US-09-864-761-3716

  Query Match             50.2%;  Score 25.6;  DB 9;  Length 416;
  Best Local Similarity   77.5%;  Pred. No. 3.3;
  Matches   31;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          5 GAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTG 44
              |||  | || |  |||||||||| |||| ||| |||||||
Db        337 GAGCAAACGTGAAGGGGAAAGCCACTGCAGCCGTGGTGTG 298


RESULT 12
US-09-864-761-1826
; Sequence 1826, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1826
;   LENGTH: 464
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC009297.2
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =   2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL =   5
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL =  22
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 9.8
US-09-864-761-1826

  Query Match             50.2%;  Score 25.6;  DB 9;  Length 464;
  Best Local Similarity   70.8%;  Pred. No. 3.3;
  Matches   34;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          3 CAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTC 50
              ||  | ||| ||||||||||    |||||||| | ||| ||  || ||
Db        269 CATGGCCAGTGAGTTGGGGATCAGCTCTGCTGTCTTGGAGTTGCCGTC 316
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RESULT 13
US-10-027-632-86806/c
; Sequence 86806, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86806
;   LENGTH: 1082
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1082)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-86806

  Query Match             50.2%;  Score 25.6;  DB 13;  Length 1082;
  Best Local Similarity   77.5%;  Pred. No. 3.4;
  Matches   31;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          5 GAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTG 44
              |||  | || |  |||||||||| |||| ||| |||||||
Db       1035 GAGCAAACGTGAAGGGGAAAGCCACTGCAGCCGTGGTGTG 996


RESULT 14
US-10-027-632-86806/c
; Sequence 86806, Application US/10027632
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86806
;   LENGTH: 1082
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1082)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-86806

  Query Match             50.2%;  Score 25.6;  DB 14;  Length 1082;
  Best Local Similarity   77.5%;  Pred. No. 3.4;
  Matches   31;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          5 GAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTG 44
              |||  | || |  |||||||||| |||| ||| |||||||
Db       1035 GAGCAAACGTGAAGGGGAAAGCCACTGCAGCCGTGGTGTG 996


RESULT 15
US-09-864-761-23584
; Sequence 23584, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23584
;   LENGTH: 426
;   TYPE: DNA
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;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL139819.2
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.7
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.4
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.1
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.5
;   OTHER INFORMATION: NT HIT: gi11434431, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: AA398511.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: P35232, EVALUE 5.00e-44
US-09-864-761-23584

  Query Match             48.6%;  Score 24.8;  DB 9;  Length 426;
  Best Local Similarity   72.7%;  Pred. No. 6.7;
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Db        188 GCCAGTGAGTTGGCGATCAGCTCTGCTGCCTTGGAATCGCCCTC 231


Search completed: December 16, 2003, 19:42:38
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GenCore version 5.1.6

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	51	100.0	2224	3	US-08-477-347-2	Sequence 2, Appli
	2	51	100.0	2224	3	US-08-476-862-1	Sequence 1, Appli
	3	51	100.0	2224	4	US-09-800-909-1	Sequence 1, Appli
	4	51	100.0	3683	4	US-09-844-634-3	Sequence 3, Appli
	5	47.8	93.7	15602	4	US-09-844-634-17	Sequence 17, Appl
c	6	23.2	45.5	1020	1	US-08-114-461-1	Sequence 1, Appli
c	7	23.2	45.5	1020	1	US-08-192-156-1	Sequence 1, Appli
c	8	23.2	45.5	1020	1	US-08-370-789-1	Sequence 1, Appli
c	9	23.2	45.5	1328	4	US-09-297-911-22	Sequence 22, Appl
	10	22.8	44.7	1128	4	US-09-252-991A-3879	Sequence 3879, Ap
c	11	22.8	44.7	1896	4	US-09-252-991A-3975	Sequence 3975, Ap
c	12	22.8	44.7	2562	4	US-09-252-991A-4045	Sequence 4045, Ap
c	13	22.4	43.9	1230	4	US-09-370-950C-1	Sequence 1, Appli
c	14	22.4	43.9	1319	2	US-08-484-993B-17	Sequence 17, Appl
c	15	22.4	43.9	1319	2	US-08-484-158B-17	Sequence 17, Appl
c	16	22.4	43.9	1319	2	US-08-484-596A-17	Sequence 17, Appl
c	17	22.4	43.9	1319	2	US-08-480-150A-17	Sequence 17, Appl
c	18	22.4	43.9	1319	3	US-08-458-731-17	Sequence 17, Appl
c	19	22.4	43.9	1319	3	US-08-149-223A-17	Sequence 17, Appl
	20	22.4	43.9	1230025	4	US-09-198-452A-1	Sequence 1, Appli
	21	22.2	43.5	1074	1	US-08-045-269C-3	Sequence 3, Appli
	22	22.2	43.5	1074	3	US-08-371-680-3	Sequence 3, Appli
	23	22.2	43.5	1074	5	PCT-US94-01198-3	Sequence 3, Appli
	24	22.2	43.5	1554	1	US-08-045-269C-1	Sequence 1, Appli
	25	22.2	43.5	1554	3	US-08-371-680-1	Sequence 1, Appli
	26	22.2	43.5	1554	5	PCT-US94-01198-1	Sequence 1, Appli
	27	22.2	43.5	536165	4	US-09-214-808-1	Sequence 1, Appli
	28	22	43.1	1530	4	US-09-252-991A-6611	Sequence 6611, Ap
	29	22	43.1	38494	4	US-08-311-731A-24	Sequence 24, Appl
	30	22	43.1	38675	4	US-08-311-731A-135	Sequence 135, App
	31	22	43.1	87563	4	US-09-453-702B-57	Sequence 57, Appl
	32	21.8	42.7	1011	2	US-09-013-634-3	Sequence 3, Appli
	33	21.8	42.7	2581	2	US-09-013-634-1	Sequence 1, Appli
c	34	21.8	42.7	2908	4	US-09-930-181-1	Sequence 1, Appli
	35	21.8	42.7	26664	4	US-09-564-805-28	Sequence 28, Appl
c	36	21.6	42.4	812	1	US-07-612-674-3	Sequence 3, Appli
c	37	21.6	42.4	1650	4	US-09-252-991A-3625	Sequence 3625, Ap
c	38	21.6	42.4	1696	1	US-07-612-674-1	Sequence 1, Appli
	39	21.6	42.4	2766	4	US-09-252-991A-3756	Sequence 3756, Ap
	40	21.6	42.4	2874	4	US-09-252-991A-3837	Sequence 3837, Ap
	41	21.4	42.0	2053	4	US-09-227-357-45	Sequence 45, Appl
c	42	21.4	42.0	2136	4	US-09-587-184-1	Sequence 1, Appli
	43	21.2	41.6	544	2	US-08-890-980-17	Sequence 17, Appl
	44	21.2	41.6	544	3	US-08-890-979-17	Sequence 17, Appl
	45	21.2	41.6	544	3	US-09-032-894-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-477-347-2
; Sequence 2, Application US/08477347
; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,347
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/115,685
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

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;      LOCATION:  90..1472
US-08-477-347-2

  Query Match             100.0%;  Score 51;  DB 3;  Length 2224;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-10;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 2
US-08-476-862-1
; Sequence 1, Application US/08476862
; Patent No. 6262239
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BIGDA, Jacek
;    APPLICANT:  BELETSKY, Igor
;    APPLICANT:  METT, Igor
;    APPLICANT:  ENGELMANN, Hartmut
;    TITLE OF INVENTION:  TNF INHIBITORS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,862
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 107267
;      FILING DATE:  12-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 94039
;      FILING DATE:  06-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 91229
;      FILING DATE:  06-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 90339
;      FILING DATE:  18-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=12A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2224 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1472
US-08-476-862-1

  Query Match             100.0%;  Score 51;  DB 3;  Length 2224;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-10;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 3
US-09-800-909-1
; Sequence 1, Application US/09800909
; Patent No. 6555111
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BIGDA, Jacek
;    APPLICANT:  BELETSKY, Igor
;    APPLICANT:  METT, Igor
;    APPLICANT:  ENGELMANN, Hartmut
;    TITLE OF INVENTION:  TNF INHIBITORS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/800,909
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/476,862
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 94039
;      FILING DATE:  06-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 91229
;      FILING DATE:  06-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 90339
;      FILING DATE:  18-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=12A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2224 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1472
US-09-800-909-1

  Query Match             100.0%;  Score 51;  DB 4;  Length 2224;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-10;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700
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RESULT 4
US-09-844-634-3
; Sequence 3, Application US/09844634
; Patent No. 6410324
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRESSI
;  FILE REFERENCE: RTS-0216
;  CURRENT APPLICATION NUMBER: US/09/844,634
;  CURRENT FILING DATE:  2001-04-27
;  NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 3
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (90)...(1475)
US-09-844-634-3

  Query Match             100.0%;  Score 51;  DB 4;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-10;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 5
US-09-844-634-17
; Sequence 17, Application US/09844634
; Patent No. 6410324
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRESSI
;  FILE REFERENCE: RTS-0216
;  CURRENT APPLICATION NUMBER: US/09/844,634
;  CURRENT FILING DATE:  2001-04-27
;  NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 17
;   LENGTH: 15602
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-844-634-17

  Query Match             93.7%;  Score 47.8;  DB 4;  Length 15602;
  Best Local Similarity   96.1%;  Pred. No. 7.3e-09;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||| |||||||||||||||||| ||||||||||
Db      11183 AGCAGAGGCAGCGAGTTGTGGAAAGCCTCTGCTGCCATGGCGTGTCCCTCT 11233


RESULT 6
US-08-114-461-1/c
; Sequence 1, Application US/08114461
; Patent No. 5401635
;  GENERAL INFORMATION:
;    APPLICANT:  NAKAMURA, Y., SATO, T.
;    TITLE OF INVENTION:  HUMAN PROHIBITIN AND DNA
;    TITLE OF INVENTION:  CODING FOR THE SAME
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLYNN, THIEL, BOUTELL & TANIS, P.C.
;      STREET:  2026 Rambling Road
;      CITY:  Kalamazoo
;      STATE:  Michigan
;      COUNTRY:  USA
;      ZIP:  49008-1699
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inches, 1.44 Mb storage
;      COMPUTER:  IBM/PC/XT/AT Compatible
;      OPERATING SYSTEM:  MS-DOS 5.0
;      SOFTWARE:  WORD PERFECT 5.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/114,461
;      FILING DATE:  31-AUG-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/009,255
;      FILING DATE:  January 22, 1993
;      APPLICATION NUMBER:  JP4-011156
;      FILING DATE:  24-01-1992
;      APPLICATION NUMBER:  JP4-308654
;      FILING DATE:  18-11-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Terryence F. Chapman
;      REGISTRATION NUMBER:  32 549
;      REFERENCE/DOCKET NUMBER:  Furuya Case 1282
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (616) 381-1156
;      TELEFAX:  (616) 381-5465
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1020 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  yes
;    ANTI-SENSE:  no
;    ORIGINAL SOURCE:
;      ORGANISM:  Homosapiens
;      INDIVIDUAL ISOLATE:
;      CELL TYPE:
;    IMMEDIATE SOURCE:
;      LIBRARY:  Human fetal brain cDNA library
;      CLONE:
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  23 to 839
;      IDENTIFICATION METHOD:  analogy with a known sequence or a consensus sequence
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:  1: FROM 1 TO 1020
US-08-114-461-1

  Query Match             45.5%;  Score 23.2;  DB 1;  Length 1020;
  Best Local Similarity   70.5%;  Pred. No. 7.9;
  Matches   31;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          7 GGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTC 50
              | ||| |||||||  |    ||| |||||| ||| ||  |||||
Db        736 GCCAGTGAGTTGGCAATCAGCTCAGCTGCCTTGGAGTCGCCCTC 693


RESULT 7
US-08-192-156-1/c
; Sequence 1, Application US/08192156
; Patent No. 5463026
;  GENERAL INFORMATION:
;    APPLICANT:  NAKAMURA, Y., SATO, T.
```

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;    TITLE OF INVENTION:  HUMAN PROHIBITIN AND DNA
;    TITLE OF INVENTION:  CODING FOR THE SAME
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLYNN, THIEL, BOUTELL & TANIS, P.C.
;      STREET:  2026 Rambling Road
;      CITY:  Kalamazoo
;      STATE:  Michigan
;      COUNTRY:  USA
;      ZIP:  49008-1699
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inches, 1.44 Mb storage
;      COMPUTER:  IBM/PC/XT/AT Compatible
;      OPERATING SYSTEM:  MS-DOS 5.0
;      SOFTWARE:  WORD PERFECT 5.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/192,156
;      FILING DATE:  04-FEB-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/009,255
;      FILING DATE:  January 22, 1993
;      APPLICATION NUMBER:  JP4-011156
;      FILING DATE:  24-01-1992
;      APPLICATION NUMBER:  JP4-308654
;      FILING DATE:  18-11-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Terryence F. Chapman
;      REGISTRATION NUMBER:  32 549
;      REFERENCE/DOCKET NUMBER:  Furuya Case 1282
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (616) 381-1156
;      TELEFAX:  (616) 381-5465
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1020 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  yes
;    ANTI-SENSE:  no
;    ORIGINAL SOURCE:
;      ORGANISM:  Homosapiens
;      INDIVIDUAL ISOLATE:
;      CELL TYPE:
;    IMMEDIATE SOURCE:
;      LIBRARY:  Human fetal brain cDNA library
;      CLONE:
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  23 to 839
;      IDENTIFICATION METHOD:  analogy with a known sequence or
;      IDENTIFICATION METHOD:  a consensus sequence
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:  1: FROM 1 TO 1020
US-08-192-156-1

  Query Match            45.5%;  Score 23.2;  DB 1;  Length 1020;
  Best Local Similarity  70.5%;  Pred. No. 7.9;
  Matches   31;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          7 GGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTC 50
              | ||| |||||||  |    ||| |||||| ||| ||  |||||
Db        736 GCCAGTGAGTTGGCAATCAGCTCAGCTGCCTTGGAGTCGCCCTC 693
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RESULT 8
US-08-370-789-1/c
; Sequence 1, Application US/08370789
; Patent No. 5599707
;  GENERAL INFORMATION:
;    APPLICANT:  NAKAMURA, Y., SATO, T.
;    TITLE OF INVENTION:  HUMAN PROHIBITIN AND DNA
;    TITLE OF INVENTION:  CODING FOR THE SAME
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLYNN, THIEL, BOUTELL & TANIS, P.C.
;      STREET:  2026 Rambling Road
;      CITY:  Kalamazoo
;      STATE:  Michigan
;      COUNTRY:  USA
;      ZIP:  49008-1699
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inches, 1.44 Mb storage
;      COMPUTER:  IBM/PC/XT/AT Compatible
;      OPERATING SYSTEM:  MS-DOS 5.0
;      SOFTWARE:  WORD PERFECT 5.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/370,789
;      FILING DATE:  10-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/114,461
;      FILING DATE:  31-AUG-1993
;      APPLICATION NUMBER:  US/08/009,255
;      FILING DATE:  January 22, 1993
;      APPLICATION NUMBER:  JP4-011156
;      FILING DATE:  24-01-1992
;      APPLICATION NUMBER:  JP4-308654
;      FILING DATE:  18-11-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Terryence F. Chapman
;      REGISTRATION NUMBER:  32 549
;      REFERENCE/DOCKET NUMBER:  Furuya Case 1282
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (616) 381-1156
;      TELEFAX:  (616) 381-5465
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1020 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  yes
;    ANTI-SENSE:  no
;    ORIGINAL SOURCE:
;      ORGANISM:  Homosapiens
;      INDIVIDUAL ISOLATE:
;      CELL TYPE:
;    IMMEDIATE SOURCE:
;      LIBRARY:  Human fetal brain cDNA library
;      CLONE:
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  23 to 839
;      IDENTIFICATION METHOD:  analogy with a known sequence or a consensus sequence
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:  1: FROM 1 TO 1020
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US-08-370-789-1

  Query Match             45.5%;  Score 23.2;  DB 1;  Length 1020;
  Best Local Similarity   70.5%;  Pred. No. 7.9;
  Matches   31;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          7 GGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTC 50
              | ||| |||||||  |    ||| |||||| ||| ||  |||||
Db        736 GCCAGTGAGTTGGCAATCAGCTCAGCTGCCTTGGAGTCGCCCTC 693


RESULT 9
US-09-297-911-22/c
; Sequence 22, Application US/09297911
; Patent No. 6355427
;  GENERAL INFORMATION:
;    APPLICANT:
;    APPLICANT:
;    APPLICANT:
;    APPLICANT:
;    APPLICANT:
;    TITLE OF INVENTION:  DIAGNOSTIC ASSAY FOR BREAST CANCER
;    TITLE OF INVENTION:  SUSCEPTIBILITY
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SIDLEY & AUSTIN
;      STREET:  717 N. Harwood, Suite 3400
;      CITY:  Dallas
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  75201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/297,911
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hansen, Eugenia S.
;      REGISTRATION NUMBER:  31,966
;      REFERENCE/DOCKET NUMBER:  11146/08308
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (214) 981-3300
;      TELEFAX:  (214) 981-3400
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1328 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  5'clip
;      LOCATION:  1..477
US-09-297-911-22

  Query Match             45.5%;  Score 23.2;  DB 4;  Length 1328;
  Best Local Similarity   70.5%;  Pred. No. 8.3;
  Matches   31;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          7 GGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTC 50
              | ||| |||||||  |    ||| |||||| ||| ||  |||||
Db        261 GCCAGTGAGTTGGCAATCAGCTCAGCTGCCTTGGAGTCGCCCTC 218


RESULT 10
US-09-252-991A-3879
; Sequence 3879, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 3879
;   LENGTH: 1128
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3879

  Query Match             44.7%;  Score 22.8;  DB 4;  Length 1128;
  Best Local Similarity   71.4%;  Pred. No. 11;
  Matches   30;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          2 GCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGT 43
              | | |||| | || || ||||| ||| ||  ||||| ||| |
Db        983 GGATAGGCGGTGATTTCGGGAATGCCGCTCATGCCACGGTCT 1024


RESULT 11
US-09-252-991A-3975/c
; Sequence 3975, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 3975
;   LENGTH: 1896
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3975

  Query Match             44.7%;  Score 22.8;  DB 4;  Length 1896;
  Best Local Similarity   71.4%;  Pred. No. 13;
  Matches   30;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          2 GCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGT 43
              | | |||| | || || ||||| ||| ||  ||||| ||| |
Db       1304 GGATAGGCGGTGATTTCGGGAATGCCGCTCATGCCACGGTCT 1263


RESULT 12
US-09-252-991A-4045/c
; Sequence 4045, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
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; SEQ ID NO 4045
;   LENGTH: 2562
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4045

  Query Match             44.7%;  Score 22.8;  DB 4;  Length 2562;
  Best Local Similarity   71.4%;  Pred. No. 13;
  Matches   30;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          2 GCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGT 43
              | | |||| | || || ||||| ||| ||  ||||| ||| |
Db         90 GGATAGGCGGTGATTTCGGGAATGCCGCTCATGCCACGGTCT 49


RESULT 13
US-09-370-950C-1/c
; Sequence 1, Application US/09370950C
; Patent No. 6500653
; GENERAL INFORMATION:
;  APPLICANT: ABO, ARIE
;  APPLICANT:  ARONHEIM, AMI
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES WHICH RESEMBLE RHO AND WHICH
;  TITLE OF INVENTION:  INTERACT WITH CELL SIGNALING PATHWAYS AND PROTEINS
;  FILE REFERENCE: ONYX1042-US
;  CURRENT APPLICATION NUMBER: US/09/370,950C
;  CURRENT FILING DATE:  1999-08-09
;  PRIOR APPLICATION NUMBER: US 60/095,725
;  PRIOR FILING DATE: 1998-08-07
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1230
;   TYPE: DNA
;   ORGANISM: RAT Chp
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (103)..(807)
;   OTHER INFORMATION:
US-09-370-950C-1

  Query Match             43.9%;  Score 22.4;  DB 4;  Length 1230;
  Best Local Similarity   66.7%;  Pred. No. 16;
  Matches   32;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCC 48
              |||||||  | |||    ||  ||    || ||||| || ||||||||
Db        400 AGCAGAGAGAACGAAGCCGGTCAAAGTCCTCCTGCCCTGCTGTGTCCC 353


RESULT 14
US-08-484-993B-17/c
; Sequence 17, Application US/08484993B
; Patent No. 5837497
;  GENERAL INFORMATION:
;    APPLICANT:  Harris Ph.D., Jeffrey D.
;    APPLICANT:  Hsu, Kuang T.
;    APPLICANT:  Podolski, Joseph S.
;    TITLE OF INVENTION:  Materials and Methods for Immunocontraception
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,993B
;      FILING DATE:  09-NOV-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/012,990
;      FILING DATE:  29-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/973,341
;      FILING DATE:  09-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  31745
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6653
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1319 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Felis domesticus
;      DEVELOPMENTAL STAGE:  Juvenile
;      HAPLOTYPE:  Diploidy
;      TISSUE TYPE:  Ovary
;      CELL TYPE:  Oocyte
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  26..1297
US-08-484-993B-17

  Query Match             43.9%;  Score 22.4;  DB 2;  Length 1319;
  Best Local Similarity   72.5%;  Pred. No. 17;
  Matches   29;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          7 GGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTC 46
              | | |||| || |||||  | |||  ||||| ||| ||||
Db       1076 GCCTGCGATTTCGGGAAGCCATCTTGTGCCACGGTCTGTC 1037


RESULT 15
US-08-484-158B-17/c
; Sequence 17, Application US/08484158B
; Patent No. 5976545
;  GENERAL INFORMATION:
;    APPLICANT:  Harris Ph.D., Jeffrey D.
;    APPLICANT:  Hsu, Kuang T.
;    APPLICANT:  Podolski, Joseph S.
;    TITLE OF INVENTION:  Pharmaceutical Compositions for
;    TITLE OF INVENTION:  Immunocontraception
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,158B
;      FILING DATE:  07-JUNE-95
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;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/149,223
;      FILING DATE:  09-NOV-93
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/012,990
;      FILING DATE:  29-JAN-93
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/973,341
;      FILING DATE:  09-NOV-92
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  32794
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6653
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1319 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Felis domesticus
;      DEVELOPMENTAL STAGE:  Juvenile
;      HAPLOTYPE:  Diploidy
;      TISSUE TYPE:  Ovary
;      CELL TYPE:  Oocyte
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  26..1297
US-08-484-158B-17

  Query Match             43.9%;  Score 22.4;  DB 2;  Length 1319;
  Best Local Similarity   72.5%;  Pred. No. 17;
  Matches   29;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          7 GGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTC 46
              | | |||| || |||||  | |||  ||||| ||| ||||
Db       1076 GCCTGCGATTTCGGGAAGCCATCTTGTGCCACGGTCTGTC 1037


Search completed: December 16, 2003, 19:05:22
Job time : 64 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 19:05:27 ; Search time 1223 Seconds
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Title: US-09-856-937A-1_COPY_580_630
Perfect score: 51
Sequence: 1 agcagaggcagcgagttggg.....ctgccatggtgtgtccctct 51

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 20

Total number of hits satisfying chosen parameters: 25

Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

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1: gb_ba:*
2: gb_htg:*
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32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	870	11	G15915	G15915 human STS C
2	51	100.0	2224	6	AR152033	AR152033 Sequence
3	51	100.0	2224	6	AR308134	AR308134 Sequence
4	51	100.0	2253	6	A78517	A78517 Sequence 1
5	51	100.0	2613	9	HSTNFR2S10	U52165 Human tumor
6	51	100.0	3380	11	G26865	G26865 human STS S
7	51	100.0	3683	6	AR215688	AR215688 Sequence
8	51	100.0	3683	6	AX333705	AX333705 Sequence
9	51	100.0	3683	6	AX348016	AX348016 Sequence
10	51	100.0	3683	6	AX348018	AX348018 Sequence
11	51	100.0	3683	6	AX348020	AX348020 Sequence
12	51	100.0	3683	6	AX698020	AX698020 Sequence
13	51	100.0	3683	9	HUMNFR	M32315 Human tumor
14	32	62.7	2282	9	BC042167	BC042167 Homo sapi
15	32	62.7	2394	9	HUMTNFRII	M55994 Human tumor
16	32	62.7	3692	9	BC052977	BC052977 Homo sapi
17	22	43.1	23	6	AX348013	AX348013 Sequence
18	21	41.2	2339	6	A26415	A26415 cDNA fragme
19	21	41.2	3492	9	S63368	S63368 Homo sapien
20	21	41.2	15602	6	AR215702	AR215702 Sequence
21	21	41.2	45584	9	AY264804	AY264804 Homo sapi
c 22	21	41.2	115602	9	HS1118D24	AL031276 Human DNA
23	21	41.2	122105	2	AL355998	AL355998 Homo sapi
24	21	41.2	153904	2	BX510650	BX510650 Homo sapi
25	21	41.2	187877	2	AC023251	AC023251 Homo sapi

ALIGNMENTS

RESULT 1
G15915
LOCUS G15915 870 bp DNA linear STS 19-JAN-1996
DEFINITION human STS CHLC.UTR_02819_M32315.P65016 clone UTR_02819_M32315, sequence tagged site.
ACCESSION G15915
VERSION G15915.1 GI:1161804
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: UTR_02819_M32315, CHLC.UTR_02819_M32315.T36190
Contact: Dr. Jeffrey C. Murray
UofI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu

Primer A: CCCTGACTCTCTGTGACCTG
Primer B: GTCTTCATGGGTGACTCAGG
STS size: 206
PCR Profile:
denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degress C
Protocol:

```
                    Template:       30ng genomic DNA
                    Primer:         each 1.5 pmole
                    dNTPs:          each 200 uM
                    Taq Polymerase: 0.3 units
                    Total Vol:      10 ul

          Buffer:
                    MgCl2:  1.5mM
                    KCl:     50mM
                    Tris:    10mM
                    pH:     8.3

                    Prepared with primer pairs derived from M32315.
FEATURES            Location/Qualifiers
     source         1. .870
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
     STS            272. .477
     primer_bind    272. .291
     primer_bind    complement(458. .477)
BASE COUNT      157 a    246 c    279 g    188 t
ORIGIN

  Query Match           100.0%;  Score 51;  DB 11;  Length 870;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 225


RESULT 2
AR152033
LOCUS       AR152033               2224 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6232446.
ACCESSION   AR152033
VERSION     AR152033.1  GI:15118083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2224)
  AUTHORS   Wallach,D., Bigda,J., Beletsky,I., Mett,I. and Engelmann,H.
  TITLE     TNF ligands
  JOURNAL   Patent: US 6232446-A 2 15-MAY-2001;
FEATURES            Location/Qualifiers
     source         1. .2224
                    /organism="unknown"
BASE COUNT      435 a    698 c    689 g    402 t
ORIGIN

  Query Match           100.0%;  Score 51;  DB 6;  Length 2224;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 3
AR308134
LOCUS       AR308134               2224 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6555111.
ACCESSION   AR308134
VERSION     AR308134.1  GI:31699179
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2224)
  AUTHORS   Wallach,D., Bigda,J., Beletsky,I., Mett,I. and Engelmann,H.
  TITLE     Method of inhibiting the cytocidal effect of TNF with TNF
            receptor-specific antibodies
  JOURNAL   Patent: US 6555111-A 1 29-APR-2003;
FEATURES            Location/Qualifiers
     source         1. .2224
                    /organism="unknown"
BASE COUNT      435 a    698 c    689 g    402 t
ORIGIN

  Query Match           100.0%;  Score 51;  DB 6;  Length 2224;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 4
A78517
LOCUS       A78517                 2253 bp    DNA     linear   PAT 19-OCT-1999
DEFINITION  Sequence 1 from Patent EP0585939.
ACCESSION   A78517
VERSION     A78517.1  GI:6090179
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2253)
  AUTHORS   Mett,I. and Wallach,D.
  TITLE     TNF LIGANDS
  JOURNAL   Patent: EP 0585939-A 1 09-MAR-1994;
            YEDA RES & DEV (IL)
FEATURES            Location/Qualifiers
     source         1. .2253
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
     CDS            90. .1475
                    /note="unnamed protein product"
                    /codon_start=1
                    /protein_id="CAB58915.1"
                    /db_xref="GI:6090180"
                    /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
                    YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
                    DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV
                    CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
                    PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                    GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                    ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                    HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                    LGVPDAGMKPS"
BASE COUNT      440 a    709 c    698 g    406 t
ORIGIN

  Query Match           100.0%;  Score 51;  DB 6;  Length 2253;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 5
HSTNFR2S10
LOCUS       HSTNFR2S10             2613 bp    DNA     linear   PRI 31-JUL-1996
DEFINITION  Human tumor necrosis factor receptor 2 (TNFR2) gene, exon 10 and
            complete cds.
ACCESSION   U52165
VERSION     U52165.1  GI:1469539
KEYWORDS    .
```

```
SEGMENT     10 of 10
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2613)
  AUTHORS   Beltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
            LePaslier,D., Stallard,B.J., Goeddel,D.V., de Sauvage,F.J. and
            Brodeur,G.M.
  TITLE     Physical mapping and genomic structure of the human TNFR2 gene
  JOURNAL   Genomics 35 (1), 94-100 (1996)
  MEDLINE   96299745
   PUBMED   8661109
REFERENCE   2  (bases 1 to 2613)
  AUTHORS   Beltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
            LePaslier,D., Stallard,B.J., Goeddel,D.V., deSauvage,F.J. and
            Brodeur,G.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAR-1996) Christian P. Beltinger, Division of
            Oncology, ARC Rm. 902 D, Childrens's Hospital of Philadelphia, 324
            South 34th Street, Philadelphia, PA 19104-4318, USA
FEATURES             Location/Qualifiers
     source          1. .2613
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1p36.2"
     mRNA            join(U52156.1:1. .167,U52157.1:7. .106,U52158.1:114. .242,
                     U52159.1:7. .156,U52160.1:7. .100,U52161.1:95. .330,
                     U52162.1:83. .160,U52163.1:7. .41,U52164.1:7. .211,125. .2613)
                     /product="tumor necrosis factor receptor"
     CDS             join(U52156.1:90. .167,U52157.1:7. .106,U52158.1:114. .242,
                     U52159.1:7. .156,U52160.1:7. .100,U52161.1:95. .330,
                     U52162.1:83. .160,U52163.1:7. .41,U52164.1:7. .211,125. .405)
                     /codon_start=1
                     /product="tumor necrosis factor receptor"
                     /protein_id="AAC50622.1"
                     /db_xref="GI:1469541"
                     /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
                     YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
                     DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV
                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                     ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
     gene            join(U52157.1:7. .112,U52158.1:1. .248,U52159.1:1. .200,
                     U52160.1:1. .106,U52161.1:1. .336,U52162.1:1. .218,
                     U52163.1:1. .58,U52164.1:1. .234,1. .2613)
                     /gene="TNFR2"
     intron          <1. .124
                     /gene="TNFR2"
                     /number=9
     exon            125. .2613
                     /gene="TNFR2"
                     /number=10
BASE COUNT      553 a    750 c    742 g    568 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 9;  Length 2613;
  Best Local Similarity   100.0%;  Pred. No. 2e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 630


RESULT 6
G26865
LOCUS       G26865                 3380 bp    DNA     linear   STS 14-JUN-1996
DEFINITION  human STS SHGC-31494, sequence tagged site.
ACCESSION   G26865
VERSION     G26865.1  GI:1375115
KEYWORDS    STS; STS sequence; primer; sequence tagged site.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3380)
  AUTHORS   Myers,R.M.
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Richard M. Myers
            Stanford Human Genome Center (SHGC)
            Stanford University School of Medicine
            Department of Genetics, M-344, Stanford, CA 94305, USA
            Tel: 4157259687
            Fax: 4157259689
            Email: myers@shgc.stanford.edu

            Primer A: CCCCACCACTAGGACTCTGA
            Primer B: CACAGAGAGTCAGGGACTTGC
            STS size: 201
            PCR Profile:
                    Initial incubation: 94 degrees C for 90 seconds

                    Denaturation:       94 degrees C for 15 seconds
                    Annealing:          62 degrees C for 23 seconds
                    Polymerization:     72 degrees C for 30 seconds
                    PCR Cycles:         30
                    Thermal Cycler:     Perkin Elmer 9600
            Protocol:
                    Template:       25 ng
                    Primer:         each 1 uM
                    dNTPs:          each 200 uM
                    Taq Polymerase: 0.05 units/ul
                    Total Vol:      10 ul

            Buffer:
                    MgCl2:          2.5 mM
                    KCl:            50  mM
                    Tris-HCl:       20  mM
                    pH:             8.3

            Prepared with primer pairs provided by Sandoz, derived from M32315
            -- Washington University/Merck EST sequence.
FEATURES             Location/Qualifiers
     source          1. .3380
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="1"
     STS             1561. .1761
     primer_bind     1561. .1580
     primer_bind     complement(1741. .1761)
BASE COUNT      703 a    1029 c    1004 g    644 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 11;  Length 3380;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 7
AR215688
LOCUS       AR215688               3683 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 3 from patent US 6410324.
ACCESSION   AR215688
VERSION     AR215688.1  GI:23313944
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3683)
  AUTHORS   Bennett,C.F. and Watt,A.T.
  TITLE     Antisense modulation of tumor necrosis factor receptor 2 expression
  JOURNAL   Patent: US 6410324-A 3 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .3683
                     /organism="unknown"
BASE COUNT      781 a   1098 c   1086 g    718 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 8
AX333705
LOCUS       AX333705                3683 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 4214 from Patent WO0194629.
ACCESSION   AX333705
VERSION     AX333705.1  GI:18124424
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 4214 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .3683
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      781 a   1098 c   1086 g    718 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 9
AX348016
LOCUS       AX348016                3683 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 49 from Patent EP1172444.
ACCESSION   AX348016
VERSION     AX348016.1  GI:18614126
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schreiber,S., Hampe,J. and Mascheretti,S.
  TITLE     Diagnostic use of polymorphisms in the gene coding for the tnf
            receptor II and method for detecting non-responders to anti-tnf
            therapy
  JOURNAL   Patent: EP 1172444-A 49 16-JAN-2002;
            Conaris Research Institute GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .3683
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS             90. .1475
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD22795.1"
                     /db_xref="GI:18614127"
                     /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
                     YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
                     DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV
                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                     ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
     mat_peptide     156
BASE COUNT      781 a   1098 c   1086 g    718 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 10
AX348018
LOCUS       AX348018                3683 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 51 from Patent EP1172444.
ACCESSION   AX348018
VERSION     AX348018.1  GI:18614128
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schreiber,S., Hampe,J. and Mascheretti,S.
  TITLE     Diagnostic use of polymorphisms in the gene coding for the tnf
            receptor II and method for detecting non-responders to anti-tnf
            therapy
  JOURNAL   Patent: EP 1172444-A 51 16-JAN-2002;
            Conaris Research Institute GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .3683
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS             90. .1475
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD22796.1"
                     /db_xref="GI:18614129"
                     /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
                     YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
                     DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV
                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                     ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
     mat_peptide     156
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BASE COUNT      780 a   1098 c   1087 g    718 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 11
AX348020
LOCUS       AX348020               3683 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 53 from Patent EP1172444.
ACCESSION   AX348020
VERSION     AX348020.1  GI:18614130
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schreiber,S., Hampe,J. and Mascheretti,S.
  TITLE     Diagnostic use of polymorphisms in the gene coding for the tnf
            receptor II and method for detecting non-responders to anti-tnf
            therapy
  JOURNAL   Patent: EP 1172444-A 53 16-JAN-2002;
            Conaris Research Institute GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .3683
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS             90. .1475
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD22797.1"
                     /db_xref="GI:18614131"
                     /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
                     YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
                     DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV
                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASRDAVCTSTSPTRSMAPGAVHLPQ
                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                     ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
     mat_peptide     156
BASE COUNT      780 a   1098 c   1088 g    717 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 12
AX698020
LOCUS       AX698020               3683 bp    DNA     linear   PAT 02-APR-2003
DEFINITION  Sequence 1 from Patent WO03009864.
ACCESSION   AX698020
VERSION     AX698020.1  GI:29499058
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lucas,J., Dialynas,D., Briggs,K. and Scalia,A.
  TITLE     Agonists and antagonists of disomet for the treatment of metabolic
            disorders
  JOURNAL   Patent: WO 03009864-A 1 06-FEB-2003;
            GENSET SA (FR)
FEATURES             Location/Qualifiers
     source          1. .3683
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     5'UTR           1. .89
     CDS             90. .1475
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD87412.1"
                     /db_xref="GI:29499059"
                     /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
                     YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
                     DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV
                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                     ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
     3'UTR           1476. .3657
     polyA_signal    3658. .3663
BASE COUNT      781 a   1098 c   1086 g    718 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 13
HUMNFR
LOCUS       HUMNFR                 3683 bp    mRNA    linear   PRI 07-JAN-1995
DEFINITION  Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION   M32315
VERSION     M32315.1  GI:189185
KEYWORDS    c-myc proto-oncogene; necrosis factor receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3683)
  AUTHORS   Smith,C.A., Davis,T., Anderson,D., Solam,L., Beckmann,M.P.,
            Jerzy,R., Dower,S.K., Cosman,D. and Goodwin,R.G.
  TITLE     A receptor for tumor necrosis factor defines an unusual family of
            cellular and viral proteins
  JOURNAL   Science 248 (4958), 1019-1023 (1990)
  MEDLINE   90260639
   PUBMED   2160731
COMMENT     Original source text: Homo sapiens lung cDNA to mRNA.
            Draft entry and computer-readable sequence for [1] kindly submitted
            by C.A.Smith, 30-MAR-1990, for release after publication.
FEATURES             Location/Qualifiers
     source          1. .3683
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="WI26-VA4"
                     /cell_type="fibroblast"
                     /tissue_type="lung"
     gene            1. .3683
                     /gene="tnfr"
     CDS             90. .1475
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                     /gene="tnfr"
                     /codon_start=1
                     /product="tumor necrosis factor receptor"
                     /protein_id="AAA59929.1"
                     /db_xref="GI:189186"
                     /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
                     YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
                     DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV
                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                     ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
     sig_peptide     90. .155
                     /gene="tnfr"
     mat_peptide     156. .1472
                     /gene="tnfr"
                     /product="tumor necrosis factor receptor"
BASE COUNT      781 a   1098 c   1086 g    718 t
ORIGIN

  Query Match             100.0%;  Score 51;  DB 9;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 14
BC042167
LOCUS       BC042167               2282 bp    mRNA    linear   PRI 09-JAN-2003
DEFINITION  Homo sapiens, Similar to tumor necrosis factor receptor
            superfamily, member 1B, clone IMAGE:5022068, mRNA, partial cds.
ACCESSION   BC042167
VERSION     BC042167.1  GI:27503828
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2282)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JAN-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 44 Row: h Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 23312365.
FEATURES             Location/Qualifiers
     source          1. .2282
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5022068"
                     /tissue_type="Muscle, rhabdomyosarcoma"
                     /clone_lib="NIH_MGC_17"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     CDS             <1. .1375
                     /codon_start=2
                     /product="Similar to tumor necrosis factor receptor
                     superfamily, member 1B"
                     /protein_id="AAH42167.1"
                     /db_xref="GI:27503829"
                     /translation="RAQRSLERRRWAARARGREGRGQPDPARTHGARRRLGRAGRRTG
                     ALGCGARLARPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVE
                     TQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPC
                     APGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVST
                     RSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVN
                     CVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASAL
                     DRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQ
                     CSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVP
                     DAGMKPS"
BASE COUNT      459 a    706 c    708 g    409 t
ORIGIN

  Query Match             62.7%;  Score 32;  DB 9;  Length 2282;
  Best Local Similarity   100.0%;  Pred. No. 6e-07;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db       1569 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1600


RESULT 15
HUMTNFRII
LOCUS       HUMTNFRII              2394 bp    mRNA    linear   PRI 03-SEP-1994
DEFINITION  Human tumor necrosis factor receptor II (TNFrII) mRNA, complete
            cds.
ACCESSION   M55994 M38549
VERSION     M55994.1  GI:339757
KEYWORDS    glycoprotein; nerve growth factor receptor related; transmembrane
            protein; tumor necrosis factor receptor; tumor necrosis factor
            receptor II.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2394)
  AUTHORS   Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W.,
            Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L.
  TITLE     A second tumor necrosis factor receptor gene product can shed a
            naturally occurring tumor necrosis factor inhibitor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8331-8335 (1990)
  MEDLINE   91045991
   PUBMED   2172983
COMMENT     Original source text: Human histiocytic lymphoma cell line U937,
            cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .2394
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="U937"
                     /cell_type="histiocytic lymphoma"
     gene            1. .2394
                     /gene="TNFrII"
     CDS             93. .1478
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                     /gene="TNFrII"
                     /note="603. .611 and 669. .677 glycosylation site; 861. .947
                     transmembrane domain; 948. .1478 cytoplasmic domain;
                     159,,860 extracellular domain"
                     /codon_start=1
                     /evidence=experimental
                     /product="tumor necrosis factor receptor"
                     /protein_id="AAA36755.1"
                     /db_xref="GI:339758"
                     /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
                     YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
                     DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV
                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASRDAVCTSTSPTRSMAPGAVHLPQ
                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                     ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
     sig_peptide     93. .158
                     /gene="TNFrII"
                     /note="putative"
     mat_peptide     159. .1475
                     /gene="TNFrII"
                     /product="tumor necrosis factor receptor"
                     /note="putative"
BASE COUNT      484 a    743 c    739 g    428 t
ORIGIN

  Query Match             62.7%;  Score 32;  DB 9;  Length 2394;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-07;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db       1672 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1703


RESULT 16
BC052977
LOCUS       BC052977                3692 bp    mRNA    linear   PRI 09-JUN-2003
DEFINITION  Homo sapiens tumor necrosis factor receptor superfamily, member 1B,
            mRNA (cDNA clone MGC:60023 IMAGE:6198614), complete cds.
ACCESSION   BC052977
VERSION     BC052977.1  GI:31419789
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3692)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932

REFERENCE   2  (bases 1 to 3692)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 110 Row: n Column: 2
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 23312365.
FEATURES             Location/Qualifiers
     source          1. .3692
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:60023 IMAGE:6198614"
                     /tissue_type="Peripheral Nervous System, sympathetic
                     trunk"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     gene            1. .3692
                     /gene="TNFRSF1B"
                     /note="synonyms: CD120b, TNF-R-II, TNFBR, TNFR2, TNFR80,
                     p75TNFR, TBPII, TNF-R75, p75"
                     /db_xref="LocusID:7133"
                     /db_xref="MIM:191191"
     CDS             88. .1473
                     /codon_start=1
                     /product="tumor necrosis factor receptor 2, precursor"
                     /protein_id="AAH52977.1"
                     /db_xref="GI:31419790"
                     /db_xref="LocusID:7133"
                     /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
                     YYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSS
                     DQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV
                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                     ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
                     HSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
                     LGVPDAGMKPS"
BASE COUNT      791 a   1098 c   1085 g    718 t
ORIGIN

  Query Match             62.7%;  Score 32;  DB 9;  Length 3692;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-07;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db       1667 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1698


RESULT 17
AX348013
LOCUS       AX348013                23 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 46 from Patent EP1172444.
```

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ACCESSION   AX348013
VERSION     AX348013.1  GI:18614123
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schreiber,S., Hampe,J. and Mascheretti,S.
  TITLE     Diagnostic use of polymorphisms in the gene coding for the tnf
            receptor II and method for detecting non-responders to anti-tnf
            therapy
  JOURNAL   Patent: EP 1172444-A 46 16-JAN-2002;
            Conaris Research Institute GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="TET Probe#"
BASE COUNT        1 a      8 c      6 g      8 t
ORIGIN

  Query Match             43.1%;  Score 22;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 0.72;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 CCTCTGCTGCCATGGTGTGTCC 47
              ||||||||||||||||||||||
Db          1 CCTCTGCTGCCATGGTGTGTCC 22


RESULT 18
A26415
LOCUS       A26415                  2339 bp    DNA     linear   PAT 26-APR-1995
DEFINITION  cDNA fragment for (75kD TNF-BP) tumor necrosis factor binding
            protein from patent EP0417563.
ACCESSION   A26415
VERSION     A26415.1  GI:904970
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 2339)
  AUTHORS   Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
  TITLE     TNF-binding proteins
  JOURNAL   Patent: EP 0417563-A 27 20-MAR-1991;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .2339
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     CDS             <1. .1179
                     /codon_start=1
                     /transl_table=11
                     /product="75kD TNF-BP"
                     /protein_id="CAA01806.1"
                     /db_xref="GI:904971"
                     /translation="SDSVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQ
                     NRICTCRPGWYCALSKQEGCRLCAPLPKCRPGFGVARPGTETSDVVCKPCAPGTFSNT
                     TSSTDICRPHQICNVVAIPGNASRDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPS
                     PEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVK
                     KKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRN
                     QPQAPGVEASGAGEARASTGSSADSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASS
                     TMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS
                     "
BASE COUNT      494 a    720 c    685 g    440 t
ORIGIN

  Query Match             41.2%;  Score 21;  DB 6;  Length 2339;
  Best Local Similarity   100.0%;  Pred. No. 0.68;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGG 40
              |||||||||||||||||||||
Db       1372 GGAAAGCCTCTGCTGCCATGG 1392


RESULT 19
S63368
LOCUS       S63368                  3492 bp    mRNA    linear   PRI 06-MAR-2001
DEFINITION  Homo sapiens tumor necrosis factor receptor mRNA, partial cds.
ACCESSION   S63368
VERSION     S63368.1  GI:235648
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3492)
  AUTHORS   Dembic,Z., Loetscher,H., Gubler,U., Pan,Y.C., Lahm,H.W., Gentz,R.,
            Brockhaus,M. and Lesslauer,W.
  TITLE     Two human TNF receptors have similar extracellular, but distinct
            intracellular, domain sequences
  JOURNAL   Cytokine 2 (4), 231-237 (1990)
  MEDLINE   91370690
   PUBMED   1966549
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 63368] from the original journal article.
            This sequence comes from Figuare 1.
FEATURES             Location/Qualifiers
     source          1. .3492
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             <1. .1278
                     /note="75-kda; This sequence comes from Figuare 1; TNF
                     receptor"
                     /codon_start=1
                     /product="tumor necrosis factor receptor"
                     /protein_id="AAB19824.2"
                     /db_xref="GI:13236879"
                     /translation="GSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCED
                     STYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCA
                     PLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASM
                     DAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGS
                     TGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQ
                     GPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDS
                     SPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEEC
                     AFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS"
BASE COUNT      757 a   1031 c   1006 g    698 t
ORIGIN

  Query Match             41.2%;  Score 21;  DB 9;  Length 3492;
  Best Local Similarity   100.0%;  Pred. No. 0.61;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGG 40
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Db       1472 GGAAAGCCTCTGCTGCCATGG 1492


RESULT 20
AR215702
LOCUS       AR215702                15602 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 17 from patent US 6410324.
ACCESSION   AR215702
VERSION     AR215702.1  GI:23313958
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15602)
  AUTHORS   Bennett,C.F. and Watt,A.T.
  TITLE     Antisense modulation of tumor necrosis factor receptor 2 expression
```

```
  JOURNAL   Patent: US 6410324-A 17 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .15602
                     /organism="unknown"
BASE COUNT     3439 a   4290 c   4227 g   3646 t
ORIGIN

  Query Match             41.2%;  Score 21;  DB 6;  Length 15602;
  Best Local Similarity   100.0%;  Pred. No. 0.39;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGG 40
              |||||||||||||||||||||
Db      11202 GGAAAGCCTCTGCTGCCATGG 11222


RESULT 21
AY264804
LOCUS       AY264804               45584 bp    DNA     linear   PRI 10-APR-2003
DEFINITION  Homo sapiens tumor necrosis factor receptor superfamily, member 1B
            (TNFRSF1B) gene, complete cds.
ACCESSION   AY264804
VERSION     AY264804.1  GI:29725899
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 45584)
  AUTHORS   Rieder,M.J., Livingston,R.J., Daniels,M.R., Chung,M.-W.,
            Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L., Robertson,P.D.,
            Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and Nickerson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAR-2003) Genome Sciences, University of Washington,
            1705 NE Pacific, Seattle, WA 98195, USA
COMMENT     To cite this work please use:  NIEHS-SNPs, Environmental Genome
            Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
            (URL: http://egp.gs.washington.edu).
FEATURES             Location/Qualifiers
     source          1. .45584
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     repeat_region   140. .271
                     /rpt_family="L2"
                     /rpt_type=dispersed
     variation       219
                     /frequency="0.01"
                     /replace="c"
     variation       225
                     /frequency="0.12"
                     /replace="a"
     variation       248
                     /frequency="0.03"
                     /replace="t"
     variation       249
                     /frequency="0.04"
                     /replace="a"
     variation       779. .795
                     /frequency="0.01"
                     /replace=""
     variation       793
                     /frequency="0.01"
                     /replace="c"
     variation       807
                     /frequency="0.01"
                     /replace="c"
     variation       842
                     /frequency="0.02"
                     /replace="c"
     repeat_region   1184. .1217
                     /rpt_family="MIR"
                     /rpt_type=dispersed
     repeat_region   1224. .1521
                     /rpt_family="Alu"
                     /rpt_type=dispersed
     variation       1261
                     /frequency="0.01"
                     /replace="a"
     variation       1550
                     /frequency="0.02"
                     /replace="g"
     variation       1596
                     /frequency="0.03"
                     /replace="a"
     variation       1626
                     /frequency="0.01"
                     /replace="t"
     variation       1692. .1706
                     /frequency="0.25"
                     /replace=""
     variation       1815. .1834
                     /frequency="0.99"
                     /replace=""
     variation       1847. .1849
                     /frequency="0.97"
                     /replace=""
     gene            1962. .44212
                     /gene="TNFRSF1B"
     mRNA            join(1962. .2136,23759. .23858,25920. .26048,26756. .26905,
                     27413. .27506,27845. .28080,28937. .29014,29566. .29600,
                     36951. .37155,41724. .44212)
                     /gene="TNFRSF1B"
                     /product="tumor necrosis factor receptor superfamily,
                     member 1B"
     variation       1976
                     /gene="TNFRSF1B"
                     /frequency="0.01"
                     /replace="t"
     variation       1992
                     /gene="TNFRSF1B"
                     /frequency="0.01"
                     /replace="t"
     variation       2023. .2030
                     /gene="TNFRSF1B"
                     /frequency="0.98"
                     /replace=""
     CDS             join(2059. .2136,23759. .23858,25920. .26048,26756. .26905,
                     27413. .27506,27845. .28080,28937. .29014,29566. .29600,
                     36951. .37155,41724. .42004)
                     /gene="TNFRSF1B"
                     /codon_start=1
                     /product="tumor necrosis factor receptor superfamily,
                     member 1B"
                     /protein_id="AAO89076.1"
                     /db_xref="GI:29725900"
                     /translation="MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLRE
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                     CKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
                     PVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                     GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESS
                     ASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD
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                     LGVPDAGMKPS"
     variation       2212
                     /gene="TNFRSF1B"
                     /frequency="0.02"
                     /replace="g"
     variation       2286
                     /gene="TNFRSF1B"
                     /frequency="0.01"
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                     /frequency="0.02"
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                /replace="c"
variation       2775
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                /frequency="0.01"
                /replace="g"
variation       2781
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                /frequency="0.01"
                /replace="g"
variation       3143
                /gene="TNFRSF1B"
                /frequency="0.01"
                /replace="a"
variation       3224
                /gene="TNFRSF1B"
                /frequency="0.01"
                /replace="a"
misc_feature    3470. .7483
                /gene="TNFRSF1B"
                /note="Region not scanned for variation"
repeat_region   3662. .3856
                /rpt_family="L2"
                /rpt_type=dispersed
repeat_region   4270. .4489
                /rpt_family="MIR"
                /rpt_type=dispersed
repeat_region   5629. .5939
                /rpt_family="Alu"
                /rpt_type=dispersed
repeat_region   5955. .6277
                /rpt_family="Alu"
                /rpt_type=dispersed
repeat_region   6300. .6606
                /rpt_family="L2"
                /rpt_type=dispersed
repeat_region   6607. .6802
                /rpt_family="MER1_type"
                /rpt_type=dispersed
repeat_region   6803. .6849
                /rpt_family="L2"
                /rpt_type=dispersed
repeat_region   7234. .7391
                /rpt_family="MIR"
                /rpt_type=dispersed
variation       7713
                /gene="TNFRSF1B"
                /frequency="0.35"
                /replace="c"
variation       7867
                /gene="TNFRSF1B"
                /frequency="0.01"
                /replace="a"
variation       7905
                /gene="TNFRSF1B"
                /frequency="0.01"
                /replace="t"
variation       7915
                /gene="TNFRSF1B"
                /frequency="0.02"
                /replace="t"
variation       7968
                /gene="TNFRSF1B"
                /frequency="0.06"
                /replace="a"
repeat_region   8024. .8163
                /rpt_family="MIR"
                /rpt_type=dispersed
variation       8211
                /gene="TNFRSF1B"
                /frequency="0.01"
                /replace="t"
variation       8574
```

```
  Query Match             41.2%;  Score 21;  DB 9;  Length 45584;
  Best Local Similarity   100.0%;  Pred. No. 0.29;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          20 GGAAAGCCTCTGCTGCCATGG 40
               |||||||||||||||||||||
Db       42198 GGAAAGCCTCTGCTGCCATGG 42218


RESULT 22
HS1118D24/c
LOCUS       HS1118D24             115602 bp    DNA     linear   PRI 04-MAR-2003
DEFINITION  Human DNA sequence from clone RP5-1118D24 on chromosome
            1p36.11-36.33, complete sequence.
ACCESSION   AL031276
VERSION     AL031276.1  GI:3947780
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 115602)
  AUTHORS   Heath,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Dec 2, 1998 this sequence version replaced gi:3724207.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest, except on the rare
            occasion of the clone being a YAC.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr1
            RP5-1118D24 is from the library RPCI-5 constructed by the group of
            Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pCYPAC2.
FEATURES             Location/Qualifiers
     source          1. .115602
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="RZPD:RPCIP704D241118"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="p36.11-36.33"
                     /clone="RP5-1118D24"
                     /clone_lib="RPCI-5"
BASE COUNT    34070 a  26789 c  25300 g  29443 t
ORIGIN
```

```
  Query Match             41.2%;  Score 21;  DB 9;  Length 115602;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          20 GGAAAGCCTCTGCTGCCATGG 40
               |||||||||||||||||||||
Db      104401 GGAAAGCCTCTGCTGCCATGG 104381


RESULT 23
AL355998
LOCUS       AL355998               122105 bp    DNA     linear   HTG 07-SEP-2001
DEFINITION  Homo sapiens chromosome 1 clone RP5-1125M11, *** SEQUENCING IN
            PROGRESS ***.
ACCESSION   AL355998
VERSION     AL355998.9  GI:15523662
KEYWORDS    HTG; HTGS_PHASE2; HTGS_CANCELLED.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Smith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Sep 7, 2001 this sequence version replaced gi:13897067.
            -------------- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: dJ1125M11
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 121044 bases at least Q40
            Consensus quality: 121310 bases at least Q30
            Consensus quality: 121451 bases at least Q20
            Insert size: 122105; sum-of-contigs
            Insert size: 142339; 6.8% error; agarose-fp
            Quality coverage: 8.74x in Q20 bases; sum-of-contigs Quality
            coverage: 7.58x in Q20 bases; agarose-fp
            --------------.
            * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
FEATURES             Location/Qualifiers
     source          1. .122105
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /clone="RP5-1125M11"
                     /clone_lib="RPCI-5"
     misc_feature    1. .122105
                     /note="assembly_fragment:02659"
BASE COUNT    27894 a  31136 c  32658 g  30417 t
ORIGIN

  Query Match             41.2%;  Score 21;  DB 2;  Length 122105;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          20 GGAAAGCCTCTGCTGCCATGG 40
               |||||||||||||||||||||
Db      114825 GGAAAGCCTCTGCTGCCATGG 114845


RESULT 24
BX510650
LOCUS       BX510650               153904 bp    DNA     linear   HTG 15-MAY-2003
DEFINITION  Homo sapiens chromosome 1 clone RP11-26G7, *** SEQUENCING IN
            PROGRESS ***, 15 unordered pieces.
ACCESSION   BX510650
VERSION     BX510650.2  GI:30840317
KEYWORDS    HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 153904)
  AUTHORS   McLay,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On May 16, 2003 this sequence version replaced gi:30722033.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bA26G7
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Chemistry: Dye-terminator; 100% of reads
            Consensus quality: 147937 bases at least Q40
            Consensus quality: 148717 bases at least Q30
            Consensus quality: 149207 bases at least Q20
            Insert size: 152504; sum-of-contigs
            Insert size: 162837; 8.8% error; agarose-fp
            Quality coverage: 6.71x in Q20 bases; sum-of-contigs Quality
            coverage: 6.61x in Q20 bases; agarose-fp
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 15 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    16251: contig of 16251 bp in length
            *    16252    16351: gap of 100 bp
            *    16352    20265: contig of 3914 bp in length
            *    20266    20365: gap of 100 bp
            *    20366    27411: contig of 7046 bp in length
            *    27412    27511: gap of 100 bp
            *    27512    32290: contig of 4779 bp in length
            *    32291    32390: gap of 100 bp
            *    32391    34723: contig of 2333 bp in length
            *    34724    34823: gap of 100 bp
            *    34824    37675: contig of 2852 bp in length
            *    37676    37775: gap of 100 bp
            *    37776    45873: contig of 8098 bp in length
            *    45874    45973: gap of 100 bp
            *    45974    51965: contig of 5992 bp in length
            *    51966    52065: gap of 100 bp
            *    52066    56024: contig of 3959 bp in length
            *    56025    56124: gap of 100 bp
            *    56125    71177: contig of 15053 bp in length
            *    71178    71277: gap of 100 bp
            *    71278    73321: contig of 2044 bp in length
            *    73322    73421: gap of 100 bp
            *    73422    76842: contig of 3421 bp in length
            *    76843    76942: gap of 100 bp
            *    76943    81348: contig of 4406 bp in length
            *    81349    81448: gap of 100 bp
            *    81449   137011: contig of 55563 bp in length
```

```
           *   137012   137111: gap of 100 bp
           *   137112   153904: contig of 16793 bp in length.
FEATURES             Location/Qualifiers
     source          1. .153904
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /clone="RP11-26G7"
                     /clone_lib="RPCI-11.1"
     misc_feature    1. .16251
                     /note="assembly_fragment:00249
                     fragment_chain:1
                     clone_end:SP6
                     vector_side:left"
     misc_feature    16352. .20265
                     /note="assembly_fragment:00234
                     fragment_chain:1"
     misc_feature    20366. .27411
                     /note="assembly_fragment:01828
                     fragment_chain:2"
     misc_feature    27512. .32290
                     /note="assembly_fragment:02578
                     fragment_chain:2"
     misc_feature    32391. .34723
                     /note="assembly_fragment:02283
                     fragment_chain:2"
     misc_feature    34824. .37675
                     /note="assembly_fragment:00610
                     fragment_chain:2"
     misc_feature    37776. .45873
                     /note="assembly_fragment:02121
                     fragment_chain:2"
     misc_feature    45974. .51965
                     /note="assembly_fragment:00725
                     fragment_chain:2"
     misc_feature    52066. .56024
                     /note="assembly_fragment:02142
                     fragment_chain:2"
     misc_feature    56125. .71177
                     /note="assembly_fragment:02132
                     fragment_chain:2"
     misc_feature    71278. .73321
                     /note="assembly_fragment:00756
                     fragment_chain:3"
     misc_feature    73422. .76842
                     /note="assembly_fragment:00555
                     fragment_chain:3"
     misc_feature    76943. .81348
                     /note="assembly_fragment:00780"
     misc_feature    81449. .137011
                     /note="assembly_fragment:01529
                     fragment_chain:4"
     misc_feature    137112. .153904
                     /note="assembly_fragment:01075
                     fragment_chain:4
                     clone_end:T7
                     vector_side:right"
BASE COUNT    37724 a  34999 c  37631 g  42135 t   1415 others
ORIGIN

  Query Match             41.2%;  Score 21;  DB 2;  Length 153904;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGG 40
              |||||||||||||||||||||
Db      61301 GGAAAGCCTCTGCTGCCATGG 61321


RESULT 25
AC023251
LOCUS       AC023251               187877 bp    DNA     linear   HTG 24-AUG-2002
DEFINITION  Homo sapiens chromosome 1 clone RP11-353D18 map 1, WORKING DRAFT
            SEQUENCE, 25 unordered pieces.
ACCESSION   AC023251
VERSION     AC023251.3  GI:8076833
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 187877)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 1, clone RP11-353D18
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 187877)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
            DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
            Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
            Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
            Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
            McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
            Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
            Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
            Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-FEB-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 187877)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
            Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
            Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
            Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
            Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
            McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
            Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
            Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
            Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
            Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On May 25, 2000 this sequence version replaced gi:7139786.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L6342
                Center clone name: 353_D_18
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
```

```
     Chemistry: Dye-terminator Big Dye; 100% of reads
     Assembly program: Phrap; version 0.960731
     Consensus quality: 177330 bases at least Q40
     Consensus quality: 182502 bases at least Q30
     Consensus quality: 184382 bases at least Q20
     Insert size: 188000; agarose-fp
     Insert size: 185477; sum-of-contigs
     Quality coverage: 4.9 in Q20 bases; agarose-fp
     Quality coverage: 4.9 in Q20 bases; sum-of-contigs
-------------.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*         1     1587: contig of 1587 bp in length
*      1588     1687: gap of 100 bp
*      1688     3808: contig of 2121 bp in length
*      3809     3908: gap of 100 bp
*      3909     6391: contig of 2483 bp in length
*      6392     6491: gap of 100 bp
*      6492     8438: contig of 1947 bp in length
*      8439     8538: gap of 100 bp
*      8539    11095: contig of 2557 bp in length
*     11096    11195: gap of 100 bp
*     11196    14256: contig of 3061 bp in length
*     14257    14356: gap of 100 bp
*     14357    18925: contig of 4569 bp in length
*     18926    19025: gap of 100 bp
*     19026    22429: contig of 3404 bp in length
*     22430    22529: gap of 100 bp
*     22530    27710: contig of 5181 bp in length
*     27711    27810: gap of 100 bp
*     27811    33955: contig of 6145 bp in length
*     33956    34055: gap of 100 bp
*     34056    39058: contig of 5003 bp in length
*     39059    39158: gap of 100 bp
*     39159    44172: contig of 5014 bp in length
*     44173    44272: gap of 100 bp
*     44273    50808: contig of 6536 bp in length
*     50809    50908: gap of 100 bp
*     50909    57062: contig of 6154 bp in length
*     57063    57162: gap of 100 bp
*     57163    64064: contig of 6902 bp in length
*     64065    64164: gap of 100 bp
*     64165    70384: contig of 6220 bp in length
*     70385    70484: gap of 100 bp
*     70485    77931: contig of 7447 bp in length
*     77932    78031: gap of 100 bp
*     78032    85239: contig of 7208 bp in length
*     85240    85339: gap of 100 bp
*     85340    93719: contig of 8380 bp in length
*     93720    93819: gap of 100 bp
*     93820   102274: contig of 8455 bp in length
*    102275   102374: gap of 100 bp
*    102375   113890: contig of 11516 bp in length
*    113891   113990: gap of 100 bp
*    113991   124382: contig of 10392 bp in length
*    124383   124482: gap of 100 bp
*    124483   138011: contig of 13529 bp in length
*    138012   138111: gap of 100 bp
*    138112   154313: contig of 16202 bp in length
*    154314   154413: gap of 100 bp
*    154414   187877: contig of 33464 bp in length.
FEATURES             Location/Qualifiers
     source          1. .187877
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1"
                     /clone="RP11-353D18"
                     /clone_lib="RPCI-11 Human Male BAC"
     misc_feature    1. .1587
                     /note="assembly_fragment"
     misc_feature    1688. .3808
                     /note="assembly_fragment"
     misc_feature    3909. .6391
                     /note="assembly_fragment"
     misc_feature    6492. .8438
                     /note="assembly_fragment"
     misc_feature    8539. .11095
                     /note="assembly_fragment"
     misc_feature    11196. .14256
                     /note="assembly_fragment"
     misc_feature    14357. .18925
                     /note="assembly_fragment"
     misc_feature    19026. .22429
                     /note="assembly_fragment"
     misc_feature    22530. .27710
                     /note="assembly_fragment"
     misc_feature    27811. .33955
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
     misc_feature    34056. .39058
                     /note="assembly_fragment"
     misc_feature    39159. .44172
                     /note="assembly_fragment"
     misc_feature    44273. .50808
                     /note="assembly_fragment"
     misc_feature    50909. .57062
                     /note="assembly_fragment"
     misc_feature    57163. .64064
                     /note="assembly_fragment"
     misc_feature    64165. .70384
                     /note="assembly_fragment"
     misc_feature    70485. .77931
                     /note="assembly_fragment"
     misc_feature    78032. .85239
                     /note="assembly_fragment"
     misc_feature    85340. .93719
                     /note="assembly_fragment"
     misc_feature    93820. .102274
                     /note="assembly_fragment"
     misc_feature    102375. .113890
                     /note="assembly_fragment"
     misc_feature    113991. .124382
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:right"
     misc_feature    124483. .138011
                     /note="assembly_fragment"

  Query Match             41.2%;  Score 21;  DB 2;  Length 187877;
  Best Local Similarity   100.0%;  Pred. No. 0.19;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          20 GGAAAGCCTCTGCTGCCATGG 40
               |||||||||||||||||||||
Db      144518 GGAAAGCCTCTGCTGCCATGG 144538


Search completed: December 16, 2003, 20:05:36
Job time : 1226 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 19:37:07 ; Search time 1319 Seconds
(without alignments)
939.749 Million cell updates/sec

Title: US-09-856-937A-1_COPY_580_630
Perfect score: 51
Sequence: 1 agcagaggcagcgagttggg.....ctgccatggtgtgtccctct 51

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 20

Total number of hits satisfying chosen parameters: 13

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		32	62.7	372	9	AA031826	AA031826 zk14b11.r
c 2		32	62.7	735	14	CA426262	CA426262 UI-H-DF0-
3		32	62.7	760	12	BI161017	BI161017 602865227
4		32	62.7	932	12	BG829828	BG829828 602764119
5		32	62.7	974	10	BG745202	BG745202 602723532
6		32	62.7	1051	10	BF568409	BF568409 602184408
c 7		32	62.7	1053	12	BQ052282	BQ052282 AGENCOURT
8		32	62.7	1102	12	BM917316	BM917316 AGENCOURT
c 9		32	62.7	1183	10	BF569011	BF569011 602184353
10		32	62.7	2291	11	BC011844	BC011844 Homo sapi
c 11		25	49.0	337	9	AW801622	AW801622 IL5-UM006
12		22	43.1	845	12	BI160187	BI160187 602864057
c 13		21	41.2	703	14	CA308252	CA308252 UI-H-FT1-

ALIGNMENTS

RESULT 1
AA031826
LOCUS AA031826 372 bp mRNA linear EST 09-MAY-1997
DEFINITION zk14b11.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:470493 5' similar to gb:M32315 TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (HUMAN);contains element PTR5 repetitive element ;, mRNA sequence.
ACCESSION AA031826
VERSION AA031826.1 GI:1501789
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 372)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 849 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 362.
FEATURES Location/Qualifiers
source 1. .372
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3756495"
/db_xref="taxon:9606"
/clone="IMAGE:470493"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAATTCGCGGCCGCCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
BASE COUNT 51 a 122 c 102 g 97 t
ORIGIN

```
  Query Match             62.7%;  Score 32;  DB 9;  Length 372;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-06;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db        137 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 168


RESULT 2
CA426262/c
LOCUS       CA426262                735 bp    mRNA    linear   EST 07-NOV-2002
DEFINITION  UI-H-DF0-bek-n-21-0-UI.s1 NCI_CGAP_DF0 Homo sapiens cDNA clone
            UI-H-DF0-bek-n-21-0-UI 3', mRNA sequence.
ACCESSION   CA426262
VERSION     CA426262.1  GI:24788988
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 11-300, >ALU (matched compliment) 539-573, >(CAAA
            )n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-DF0-bek-n-21-0-UI"
                     /tissue_type="Subchondral Bone"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_DF0"
                     /note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_DF0 is a cDNA library containing the following
                     tissue(s): Subchondral Bone. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is GTTAAGCGTC.
                     TAG_LIB=UI-H-DF0
                     TAG_TISSUE=subchondral bone
                     TAG_SEQ=GTTAAGCGTC"
BASE COUNT      159 a    231 c    191 g    153 t      1 others
ORIGIN

  Query Match             62.7%;  Score 32;  DB 14;  Length 735;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-06;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db        716 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 685


RESULT 3
BI161017
LOCUS       BI161017                760 bp    mRNA    linear   EST 05-JUL-2001
DEFINITION  602865227F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019247 5',
            mRNA sequence.
ACCESSION   BI161017
VERSION     BI161017.1  GI:14621018
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 760)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1834  row: e  column: 08
            High quality sequence stop: 723.
FEATURES             Location/Qualifiers
     source          1. .760
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5019247"
                     /tissue_type="epithelioid carcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_42"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library. |"
BASE COUNT      143 a    248 c    245 g    124 t
ORIGIN

  Query Match             62.7%;  Score 32;  DB 12;  Length 760;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-06;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db        690 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 721


RESULT 4
BG829828
LOCUS       BG829828                932 bp    mRNA    linear   EST 22-MAY-2001
DEFINITION  602764119F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4899436 5',
            mRNA sequence.
ACCESSION   BG829828
VERSION     BG829828.1  GI:14177415
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 932)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1791  row: e  column: 05
            High quality sequence stop: 833.
FEATURES             Location/Qualifiers
     source          1. .932
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4899436"
                     /tissue_type="epithelioid carcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_42"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library. |"
BASE COUNT      162 a    296 c    296 g    177 t      1 others
ORIGIN

  Query Match             62.7%;  Score 32;  DB 12;  Length 932;
  Best Local Similarity   100.0%;  Pred. No. 3e-06;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db        691 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 722


RESULT 5
BG745202
LOCUS       BG745202                974 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602723532F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4850143 5',
            mRNA sequence.
ACCESSION   BG745202
VERSION     BG745202.1  GI:14055855
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 974)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1690  row: o  column: 08
            High quality sequence stop: 420.
FEATURES             Location/Qualifiers
     source          1. .974
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4850143"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      301 a    245 c    285 g    143 t
ORIGIN

  Query Match             62.7%;  Score 32;  DB 10;  Length 974;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db         33 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 64


RESULT 6
BF568409
LOCUS       BF568409                1051 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602184408F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300633 5',
            mRNA sequence.
ACCESSION   BF568409
VERSION     BF568409.1  GI:11641789
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1051)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1159  row: o  column: 02
            High quality sequence stop: 769.
FEATURES             Location/Qualifiers
     source          1. .1051
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4300633"
                     /tissue_type="epithelioid carcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_42"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library. |"
BASE COUNT      229 a    313 c    346 g    161 t      2 others
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ORIGIN

  Query Match             62.7%;  Score 32;  DB 10;  Length 1051;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db        690 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 721


RESULT 7
BQ052282/c
LOCUS       BQ052282                1053 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6868457 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933511
            5', mRNA sequence.
ACCESSION   BQ052282
VERSION     BQ052282.1  GI:19811622
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1053)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2118  row: c  column: 16
            High quality sequence stop: 649.
FEATURES             Location/Qualifiers
     source          1. .1053
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5933511"
                     /tissue_type="natural killer cells, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_106"
                     /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      216 a    328 c    297 g    212 t
ORIGIN

  Query Match             62.7%;  Score 32;  DB 12;  Length 1053;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db        726 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 695


RESULT 8
BM917316
LOCUS       BM917316                1102 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6606593 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5483819
            5', mRNA sequence.
ACCESSION   BM917316
VERSION     BM917316.1  GI:19367695
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1102)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2012  row: b  column: 12
            High quality sequence stop: 507.
FEATURES             Location/Qualifiers
     source          1. .1102
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5483819"
                     /tissue_type="natural killer cells, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_106"
                     /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      219 a    366 c    292 g    222 t      3 others
ORIGIN

  Query Match             62.7%;  Score 32;  DB 12;  Length 1102;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-06;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db        191 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 222


RESULT 9
BF569011/c
LOCUS       BF569011                1183 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602184353T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300500 3',
            mRNA sequence.
ACCESSION   BF569011
VERSION     BF569011.1  GI:11642391
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1183)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
```

,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 90 a 108 c 95 g 44 t
ORIGIN

Query Match 49.0%; Score 25; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 CTCTGCTGCCATGGTGTGTCCCTCT 51
||||||||||||||||||||||||||
Db 337 CTCTGCTGCCATGGTGTGTCCCTCT 313

RESULT 12
BI160187
LOCUS BI160187 845 bp mRNA linear EST 05-JUL-2001
DEFINITION 602864057F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5018007 5', mRNA sequence.
ACCESSION BI160187
VERSION BI160187.1 GI:14620188
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 845)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1831 row: a column: 16
High quality sequence stop: 845.
FEATURES Location/Qualifiers
source 1. .845
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5018007"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_42"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"
BASE COUNT 147 a 258 c 261 g 179 t
ORIGIN

Query Match 43.1%; Score 22; DB 12; Length 845;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TGCTGCCATGGTGTGTCCCTCT 51
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Db 748 TGCTGCCATGGTGTGTCCCTCT 769

RESULT 13
CA308252/c
LOCUS CA308252 703 bp mRNA linear EST 01-NOV-2002
DEFINITION UI-H-FT1-bhy-e-02-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone UI-H-FT1-bhy-e-02-0-UI 3', mRNA sequence.
ACCESSION CA308252
VERSION CA308252.1 GI:24471306
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 703)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 11-300, >ALU (matched compliment) 538-572, >(CAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .703
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhy-e-02-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT1
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"
BASE COUNT 155 a 220 c 183 g 145 t
ORIGIN

Query Match 41.2%; Score 21; DB 14; Length 703;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 GCTGCCATGGTGTGTCCCTCT 51
|||||||||||||||||||||
Db 703 GCTGCCATGGTGTGTCCCTCT 683

Search completed: December 16, 2003, 20:27:41
Job time : 1320 secs

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1159 row: i column: 13
High quality sequence stop: 716.

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FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4300500"
                     /tissue_type="epithelioid carcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_42"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library. |"
BASE COUNT      308 a    357 c    348 g    170 t
ORIGIN

  Query Match             62.7%;  Score 32;  DB 10;  Length 1183;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-06;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db        649 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 618
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```
RESULT 10
BC011844
LOCUS       BC011844                2291 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, Similar to tumor necrosis factor receptor
            superfamily, member 1B, clone IMAGE:4111730, mRNA.
ACCESSION   BC011844
VERSION     BC011844.1  GI:15080140
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2291)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUL-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.
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Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 28 Row: i Column: 15
This clone has the following problem: retained intron.

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FEATURES             Location/Qualifiers
     source          1. .2291
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     /tissue_type="Muscle, rhabdomyosarcoma"
                     /clone_lib="NIH_MGC_17"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
BASE COUNT      461 a    708 c    713 g    409 t
ORIGIN

  Query Match             62.7%;  Score 32;  DB 11;  Length 2291;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-06;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db       1578 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1609
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```
RESULT 11
AW801622/c
LOCUS       AW801622                 337 bp    mRNA    linear   EST 16-MAY-2000
DEFINITION  IL5-UM0068-080400-056-b02 UM0068 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW801622
VERSION     AW801622.1  GI:7853492
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 337)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=IL5-UM0068-080
            400-056-b02&t3=2000-04-08&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 336.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="UM0068"
                     /note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 19:04:22 ; Search time 145 Seconds
(without alignments)
949.458 Million cell updates/sec

Title: US-09-856-937A-1_COPY_580_630
Perfect score: 51
Sequence: 1 agcagaggcagcgagttggg.....ctgccatggtgtgtccctct 51

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 20

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : N_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	2224	16	AAQ89544	p75 Tumour Necrosi
2	51	100.0	2613	21	AAA49207	Human tumour necro
3	51	100.0	2613	24	ABZ35564	Human gene express
4	51	100.0	3683	24	ABZ34910	Human gene express
5	51	100.0	3683	24	ABQ74753	Human tumour necro
6	51	100.0	3683	24	ABK83997	Human cDNA differe
7	51	100.0	3683	24	ABL65877	Lung cancer relate
8	51	100.0	3683	24	ABK33465	Human TNF receptor
9	51	100.0	3683	24	ABK33466	Human TNF receptor
10	51	100.0	3683	24	ABK33467	Human TNF receptor
11	40	78.4	201	19	AAX12093	Human biallelic po
12	32	62.7	2393	12	AAQ10907	40kD TNF inhibitor
13	32	62.7	2394	22	AAC83951	Human 40 kDa TNF i
14	25	49.0	51	22	AAL29880	Human SNP oligonuc
15	22	43.1	23	24	ABK33462	Human TNF-receptor
16	21	41.2	2339	12	AAQ10956	Encodes human 75kD
17	21	41.2	2339	20	AAZ09171	Human tumour necro
18	21	41.2	2339	22	AAH48860	Human TNFBP-associ
19	21	41.2	15602	24	ABQ74767	Human TNFR2 partia

ALIGNMENTS

RESULT 1
AAQ89544
ID AAQ89544 standard; DNA; 2224 BP.
XX
AC AAQ89544;
XX
DT 25-MAR-2003 (updated)
DT 31-OCT-1995 (first entry)
XX
DE p75 Tumour Necrosis Factor Receptor.
XX
KW Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
KW receptor; ss..
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT misc_difference 1137..1139
FT /*tag= b
FT /transl_except= GCA encodes Glycine.
FT misc_difference 1140..1142
FT /*tag= c
FT /transl_except= CCA encodes Alanine.
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FT misc_difference 1170..1172
FT /*tag= k
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FT misc_difference 1173..1175
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FT misc_difference 1176..1178
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FT misc_difference 1182..1184

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FT                   /transl_except= ACC encodes Proline.
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FT                   /transl_except= AGC encodes Glycine.
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FT                   /transl_except= TCA encodes Histidine.
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FT                   /transl_except= GAT encodes Glycine.
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FT                   /transl_except= GGT encodes Proline.
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FT                   /transl_except= CAT encodes Valine.
FT   misc_difference 2015..2016
FT                   /*tag=  w
FT                   /transl_except= GGG encodes Glutamic acid.
FT   misc_difference 2017..2018
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FT                   /transl_except= ACC encodes Alanine.
FT   misc_difference 2019..2021
FT                   /*tag=  y
FT                   /transl_except= CAG encodes Serine.
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PN   EP648783-A1.
XX
PD   19-APR-1995.
XX
PF   11-OCT-1994;   94EP-0116015.
XX
PR   12-OCT-1993;   93IL-0107267.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
PA   (WALL/) WALLACH D.
XX
PI   Beletsky I,  Bigda J,  Mett I,  Wallach D;
XX
DR   WPI; 1995-148673/20.
DR   P-PSDB; AAR72504.
XX
PT   Tumour necrosis factor (TNF) receptor ligand - used to increase
PT   inhibitory effect of a soluble TNF receptor
XX
PS   Disclosure; Figure 2; 18pp; English.
XX
CC   A ligand to a member of the tumour necrosis factor (TNF)/nerve
CC   growth factor (NGF) receptor family which binds either to the region
CC   of the 4th-Cys rich domain of the receptor, or to the region between
CC   it and the cell membrane may be used in the production of a
CC   pharmaceutical composition for increasing the inhibitory effect of a
CC   soluble receptor of the TNF/NGF receptor family.  This sequence
CC   encodes the p75 TNF receptor.  N in the sequence represents an
CC   unidentified nucleotide (poor reproduction in specification).
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2224 BP; 432 A; 697 C; 688 G; 400 T; 7 other;

  Query Match             100.0%;  Score 51;  DB 16;  Length 2224;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 2
AAA49207
ID   AAA49207 standard; DNA; 2613 BP.
XX
AC   AAA49207;
XX
DT   22-NOV-2000  (first entry)
XX
DE   Human tumour necrosis factor alpha receptor 2 gene exon 10.
XX
KW   Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;
KW   osteoporosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..2613
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FT                   /product= "TNFR2"
FT                   /partial
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FT                   /*tag=  b
FT                   /label= allele_1
FT   allele          replace (593,A), (598,T), (620,T)
FT                   /*tag=  c
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FT                   /*tag=  d
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FT                   /*tag=  e
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FT                   /label= allele_5
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PN   WO200032826-A1.
XX
PD   08-JUN-2000.
XX
PF   30-NOV-1999;   99WO-US28403.
XX
PR   30-NOV-1998;   98US-0110268.
XX
PA   (UYDR-) UNIV DREXEL.
XX
PI   Spotila LD;
XX
DR   WPI; 2000-412362/35.
XX
PT   Identifying individuals at risk of developing osteoporosis comprises
PT   assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene
PT   in a DNA sample from an individual -
XX
PS   Claim 2; Page 17-18; 21pp; English.
XX
CC   The present sequence comprises exon 10 of the human tumour necrosis
CC   factor alpha receptor 2 (THFR2) gene. The sequence contains three
CC   polymorphic sites. By determining the genotype of an individual it is
CC   possible to identify those at risk of osteoporosis, which is
CC   characterised by low bone density and fragile bones, later in life. Those
CC   at greatest risk are those who possess allele 1, which is the rarest
CC   allele. This is particularly useful as many cases of osteoporosis go
CC   undetected at present.
XX
SQ   Sequence 2613 BP; 553 A; 750 C; 742 G; 568 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 21;  Length 2613;
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  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 630


RESULT 3
ABZ35564
ID   ABZ35564 standard; cDNA; 2613 BP.
XX
AC   ABZ35564;
XX
DT   05-FEB-2003  (first entry)
XX
DE   Human gene expression profile polynucleotide SEQ ID NO 675.
XX
KW   Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW   bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW   tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW   gene expression; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200274979-A2.
XX
PD   26-SEP-2002.
XX
PF   20-MAR-2002; 2002WO-US08456.
XX
PR   20-MAR-2001; 2001US-276947P.
XX
PA   (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI   Wan J,  Wang Y;
XX
DR   WPI; 2002-740862/80.
XX
PT   New gene expression profile generated from primary, endothelial,
PT   epithelial, and muscle cell types, useful for identifying disease
PT   pathologies involving alterations of gene expression, e.g. cancer  -
XX
PS   Example 3; Page 798-799; 850pp; English.
XX
CC   The invention relates to a gene expression profile comprising one or more
CC   genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
CC   is a coronary artery endothelium, umbilical artery or vein endothelium,
CC   aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC   endothelium, myometrium microvascular endothelium, keratinocyte
CC   epithelium, bronchial epithelium, mammary epithelium, prostate
CC   epithelium, renal cortical epithelium, renal proximal tubule epithelium,
CC   small airway epithelium, renal epithelium, umbilical artery smooth
CC   muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
CC   dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
CC   aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
CC   bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
CC   osteoblasts or prostate stromal cell. The gene expression profile is used
CC   for determining the level of RNA expression for a sample, determining the
CC   phenotype of a cell and distinguishing cell types. The gene or a protein
CC   expression profile is useful in identifying disease pathologies
CC   involving alterations of gene expression. The assessment of expression
CC   profiles may provide meaningful information with respect to tumour type
CC   and stage, treatment methods, and prognosis. The gene or protein
CC   expression profile may also be used for creating microarrays. The
CC   microarray is useful for genetic and physical mapping of genomes, DNA
CC   sequencing, genetic or medical diagnosis, genotyping of organisms,
CC   confirming cell or tissue identifications and in identifying promising
CC   antibiotics, antiviral or antifungal agents.
XX
SQ   Sequence 2613 BP; 553 A; 750 C; 742 G; 568 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 2613;

  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 630


RESULT 4
ABZ34910
ID   ABZ34910 standard; cDNA; 3683 BP.
XX
AC   ABZ34910;
XX
DT   05-FEB-2003  (first entry)
XX
DE   Human gene expression profile polynucleotide SEQ ID NO 22.
XX
KW   Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW   bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW   tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW   gene expression; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200274979-A2.
XX
PD   26-SEP-2002.
XX
PF   20-MAR-2002; 2002WO-US08456.
XX
PR   20-MAR-2001; 2001US-276947P.
XX
PA   (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI   Wan J,  Wang Y;
XX
DR   WPI; 2002-740862/80.
XX
PT   New gene expression profile generated from primary, endothelial,
PT   epithelial, and muscle cell types, useful for identifying disease
PT   pathologies involving alterations of gene expression, e.g. cancer  -
XX
PS   Claim 1; Page 235-236; 850pp; English.
XX
CC   The invention relates to a gene expression profile comprising one or more
CC   genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
CC   is a coronary artery endothelium, umbilical artery or vein endothelium,
CC   aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC   endothelium, myometrium microvascular endothelium, keratinocyte
CC   epithelium, bronchial epithelium, mammary epithelium, prostate
CC   epithelium, renal cortical epithelium, renal proximal tubule epithelium,
CC   small airway epithelium, renal epithelium, umbilical artery smooth
CC   muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
CC   dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
CC   aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
CC   bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
CC   osteoblasts or prostate stromal cell. The gene expression profile is used
CC   for determining the level of RNA expression for a sample, determining the
CC   phenotype of a cell and distinguishing cell types. The gene or a protein
CC   expression profile is useful in identifying disease pathologies
CC   involving alterations of gene expression. The assessment of expression
CC   profiles may provide meaningful information with respect to tumour type
CC   and stage, treatment methods, and prognosis. The gene or protein
CC   expression profile may also be used for creating microarrays. The
CC   microarray is useful for genetic and physical mapping of genomes, DNA
CC   sequencing, genetic or medical diagnosis, genotyping of organisms,
CC   confirming cell or tissue identifications and in identifying promising
CC   antibiotics, antiviral or antifungal agents.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
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  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 5
ABQ74753
ID   ABQ74753 standard; cDNA; 3683 BP.
XX
AC   ABQ74753;
XX
DT   24-OCT-2002  (first entry)
XX
DE   Human tumour necrosis factor receptor 2 encoding cDNA SEQ ID NO:3.
XX
KW   Tumour necrosis factor receptor 2; TNFR2; antisense oligonucleotide;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "tumour necrosis factor receptor 2"
XX
PN   US6410324-B1.
XX
PD   25-JUN-2002.
XX
PF   27-APR-2001; 2001US-0844634.
XX
PR   27-APR-2001; 2001US-0844634.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Watt AT;
XX
DR   WPI; 2002-606814/65.
DR   P-PSDB; ABP52451.
XX
PT   New compounds antisense to nucleic acid encoding human or mouse tumor
PT   necrosis factor receptor 2 are useful to treat disease associated with
PT   mouse tumor necrosis factor receptor 2 expression  -
XX
PS   Claim 1; Column 53-58; 69pp; English.
XX
CC   The present invention describes compounds of 8-30 nucleobases antisense
CC   to a nucleic acid encoding human or mouse tumour necrosis factor
CC   receptor 2 (TNFR2). Also described is a method for inhibiting expression
CC   of human or mouse TNFR2 comprising contacting cells or tissues in vitro
CC   with one of the claimed compounds. The antisense compounds are used to
CC   treat a disease or condition associated with expression of TNFR2. The
CC   present sequence encodes human TNFR2, which is used in an example from
CC   the present invention.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 6
ABK83997
ID   ABK83997 standard; cDNA; 3683 BP.
XX
AC   ABK83997;
XX
DT   14-AUG-2002  (first entry)
XX
DE   Human cDNA differentially expressed in granulocytic cells #568.
XX
KW   Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW   viral infection; parasitic infection; protozoal infection;
KW   fungal infection; sterile inflammatory disease; psoriasis;
KW   rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW   cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW   adult respiratory distress syndrome; inflammatory bowel disease;
KW   Crohn's disease; ulcerative colitis; periodontal disease;
KW   granulocyte activation; chronic inflammation; allergy.
XX
OS   Homo sapiens.
XX
PN   WO200228999-A2.
XX
PD   11-APR-2002.
XX
PF   03-OCT-2001; 2001WO-US30821.
XX
PR   03-OCT-2000; 2000US-237189P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Beazer-Barclay Y,  Weissman SM,  Yamaga S,  Vockley J;
XX
DR   WPI; 2002-435328/46.
XX
PT   Detecting granulocyte activation by detecting differential expression
PT   of genes associated with granulocyte activation, which serves as
PT   diagnostic markers that is useful for monitoring disease states and
PT   drug toxicity  -
XX
PS   Claim 1; SEQ ID No 568; 114pp; English.
XX
CC   The invention relates to detecting (M1) granulocyte (GC) activation
CC   (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC   DNA chip analysis as given in the specification, and comparing
CC   the expression level to an expression level in an unactivated
CC   GC, where differential expression of Gs is indicative of GCA.
CC   Also included are modulating (M2) GA by contacting GC with an agent
CC   that alters the expression of at least one gene in Gs; (2) screening (M3)
CC   for an agent capable of modulating GCA or an inflammation (especially
CC   chronic) in a tissue, an allergic response in a subject, exposure of a
CC   subject to a pathogen or sterile inflammatory disease using the
CC   gene expression profile; (3) detecting (M4) an inflammation (especially
CC   chronic) in a tissue, an allergic response in a subject, exposure of a
CC   subject to a pathogen or sterile inflammatory disease, by detecting the
CC   level of expression in a sample of the tissue of gene(s) from Gs, where
CC   the level of expression of the gene is indicative of inflammation;
CC   (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC   an allergic response in a subject, exposure of a subject to a pathogen
CC   or sterile inflammatory disease, by contacting a tissue having
CC   inflammation with an agent that modulates the expression of gene(s)
CC   from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC   modulating GA; M3 is useful for screening an agent capable of modulating
CC   GCA preferably in an inflammation in a tissue; M4 is useful for
CC   detecting an inflammation (especially chronic) in a tissue, an allergic
CC   response in a subject, exposure of a subject to a pathogen or sterile
CC   inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC   glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC   reperfusion injury, ARDS, adult respiratory distress syndrome,
CC   inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC   periodontal disease; also bacterial infection, viral infection,
CC   parasitic infection, protozoal infection, fungal infection and M5 is
CC   useful for treating one of the above conditions. The present
CC   sequence represents a gene differentially expressed in granulocytes.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
```

```
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 7
ABL65877
ID   ABL65877 standard; DNA; 3683 BP.
XX
AC   ABL65877;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Lung cancer related gene sequence SEQ ID NO:4214.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US10838.
XX
PR   05-JUN-2000; 2000US-209473P.
PR   05-JUN-2000; 2000US-209531P.
PR   18-SEP-2000; 2000US-233133P.
PR   18-SEP-2000; 2000US-233617P.
PR   20-SEP-2000; 2000US-234009P.
PR   20-SEP-2000; 2000US-234034P.
PR   20-SEP-2000; 2000US-234052P.
PR   22-SEP-2000; 2000US-234509P.
PR   22-SEP-2000; 2000US-234567P.
PR   25-SEP-2000; 2000US-234923P.
PR   25-SEP-2000; 2000US-234924P.
PR   25-SEP-2000; 2000US-235077P.
PR   25-SEP-2000; 2000US-235082P.
PR   25-SEP-2000; 2000US-235134P.
PR   25-SEP-2000; 2000US-235280P.
PR   26-SEP-2000; 2000US-235637P.
PR   26-SEP-2000; 2000US-235638P.
PR   27-SEP-2000; 2000US-235711P.
PR   27-SEP-2000; 2000US-235720P.
PR   27-SEP-2000; 2000US-235840P.
PR   27-SEP-2000; 2000US-235863P.
PR   28-SEP-2000; 2000US-236028P.
PR   28-SEP-2000; 2000US-236032P.
PR   28-SEP-2000; 2000US-236033P.
PR   28-SEP-2000; 2000US-236034P.
PR   28-SEP-2000; 2000US-236109P.
PR   28-SEP-2000; 2000US-236111P.
PR   29-SEP-2000; 2000US-236842P.
PR   29-SEP-2000; 2000US-236891P.
PR   02-OCT-2000; 2000US-237172P.
PR   02-OCT-2000; 2000US-237173P.
PR   02-OCT-2000; 2000US-237278P.
PR   02-OCT-2000; 2000US-237294P.
PR   02-OCT-2000; 2000US-237295P.
PR   02-OCT-2000; 2000US-237316P.
PR   03-OCT-2000; 2000US-237425P.
PR   03-OCT-2000; 2000US-237598P.
PR   03-OCT-2000; 2000US-237604P.
PR   03-OCT-2000; 2000US-237606P.
PR   03-OCT-2000; 2000US-237608P.
PR   01-NOV-2000; 2000US-244867P.
PR   01-NOV-2000; 2000US-245084P.
XX
PA   (AVAL-) AVALON PHARM.
XX
PI   Young PE,  Augustus M,  Carter KC,  Ebner R,  Endress G,  Horrigan S;
PI   Soppet DR,  Weaver Z;
XX
DR   WPI; 2002-188264/24.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a
PT   chemical agent to be tested for anti-neoplastic activity, and
PT   determining a change in expression of a gene of a signature gene set
XX
PS   Claim 1; SEQ ID 4214; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an
CC   anti-neoplastic agent. The method involves exposing cells to a chemical
CC   agent to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening
CC   an anti-neoplastic agent, and can be used for producing a product which
CC   is the data collected with respect to the anti-neoplastic agent as a
CC   result of M1, and the data is sufficient to convey the chemical
CC   structure and/or properties of the agent. M1 can be used in the
CC   treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC   oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC   adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC   infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC   carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 8
ABK33465
ID   ABK33465 standard; DNA; 3683 BP.
XX
AC   ABK33465;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human TNF receptor II gene.
XX
KW   Human; anti-tumour necrosis factor receptor II; TNF receptor II;
KW   chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW   inflammatory disorder; chronic disease; receptor; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "TNF receptor II"
FT   sig_peptide     90..155
FT                   /*tag=  b
FT   mat_peptide     156..1472
FT                   /*tag=  c
XX
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PN   EP1172444-A1.
XX
PD   16-JAN-2002.
XX
PF   10-JUL-2000; 2000EP-0114786.
XX
PR   10-JUL-2000; 2000EP-0114786.
XX
PA   (CONA-) CONARIS RES INST GMBH.
XX
PI   Schreiber S,  Hampe J,  Mascheretti S;
XX
DR   WPI; 2002-156651/21.
DR   P-PSDB; AAU75172.
XX
PT   Detecting non-responders to anti-human necrosis factor therapy,
PT   comprises testing an individual for homozygosity for a single
PT   nucleotide polymorphism in the gene coding for the tumour necrosis
PT   factor receptor II  -
XX
PS   Disclosure; Page 23-27; 45pp; English.
XX
CC   The present invention relates to a method for detecting non-responders
CC   to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC   an individual for homozygosity for at least one single nucleotide
CC   polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC   located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC   A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC   Met196Arg respectively, are also described. The method of the invention
CC   is useful for detecting non-responders to anti-TNF therapy such as
CC   infliximab therapy, or therapy of Crohn's disease. The genes containing
CC   the 2 novel polymorphisms are useful for diagnostic purposes in
CC   inflammatory, malignant or other chronic diseases. The present sequence
CC   encodes for human TNF receptor II.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 9
ABK33466
ID   ABK33466 standard; DNA; 3683 BP.
XX
AC   ABK33466;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human TNF receptor II gene with SNP in exon 2.
XX
KW   Human; anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
KW   chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW   inflammatory disorder; chronic disease; receptor; gene;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "TNF receptor II variant #1"
FT   sig_peptide     90..155
FT                   /*tag=  b
FT   mat_peptide     156..1472
FT                   /*tag=  c
FT   variation       replace (257, A)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   EP1172444-A1.
XX
PD   16-JAN-2002.
XX
PF   10-JUL-2000; 2000EP-0114786.
XX
PR   10-JUL-2000; 2000EP-0114786.
XX
PA   (CONA-) CONARIS RES INST GMBH.
XX
PI   Schreiber S,  Hampe J,  Mascheretti S;
XX
DR   WPI; 2002-156651/21.
DR   P-PSDB; AAU75173.
XX
PT   Detecting non-responders to anti-human necrosis factor therapy,
PT   comprises testing an individual for homozygosity for a single
PT   nucleotide polymorphism in the gene coding for the tumour necrosis
PT   factor receptor II  -
XX
PS   Claim 15; Page 29-33; 45pp; English.
XX
CC   The present invention relates to a method for detecting non-responders
CC   to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC   an individual for homozygosity for at least one single nucleotide
CC   polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC   located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC   A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC   Met196Arg respectively, are also described. The method of the invention
CC   is useful for detecting non-responders to anti-TNF therapy such as
CC   infliximab therapy, or therapy of Crohn's disease. The genes containing
CC   the 2 novel polymorphisms are useful for diagnostic purposes in
CC   inflammatory, malignant or other chronic diseases. The present sequence
CC   represents the human TNF receptor II gene containing the SNP in exon 2.
XX
SQ   Sequence 3683 BP; 780 A; 1098 C; 1087 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 10
ABK33467
ID   ABK33467 standard; DNA; 3683 BP.
XX
AC   ABK33467;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human TNF receptor II gene with SNP in exon 6.
XX
KW   Human; anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
KW   chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW   inflammatory disorder; chronic disease; receptor; gene;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "TNF receptor II variant #2"
FT   sig_peptide     90..155
FT                   /*tag=  b
FT   mat_peptide     156..1472
FT                   /*tag=  c
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FT   variation       replace (676, T)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   EP1172444-A1.
XX
PD   16-JAN-2002.
XX
PF   10-JUL-2000; 2000EP-0114786.
XX
PR   10-JUL-2000; 2000EP-0114786.
XX
PA   (CONA-) CONARIS RES INST GMBH.
XX
PI   Schreiber S,  Hampe J,  Mascheretti S;
XX
DR   WPI; 2002-156651/21.
DR   P-PSDB; AAU75174.
XX
PT   Detecting non-responders to anti-human necrosis factor therapy,
PT   comprises testing an individual for homozygosity for a single
PT   nucleotide polymorphism in the gene coding for the tumour necrosis
PT   factor receptor II  -
XX
PS   Claim 16; Page 35-39; 45pp; English.
XX
CC   The present invention relates to a method for detecting non-responders
CC   to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC   an individual for homozygosity for at least one single nucleotide
CC   polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC   located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC   A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC   Met196Arg respectively, are also described. The method of the invention
CC   is useful for detecting non-responders to anti-TNF therapy such as
CC   infliximab therapy, or therapy of Crohn's disease. The genes containing
CC   the 2 novel polymorphisms are useful for diagnostic purposes in
CC   inflammatory, malignant or other chronic diseases. The present sequence
CC   represents the human TNF receptor II gene containing the SNP in exon 6.
XX
SQ   Sequence 3683 BP; 780 A; 1098 C; 1088 G; 717 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 11
AAX12093
ID   AAX12093 standard; DNA; 201 BP.
XX
AC   AAX12093;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Human biallelic polymorphic DNA fragment M32315b.
XX
KW   Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW   detection; phenotypic typing; characteristic; infection; hereditary;
KW   autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW   treatment; marker; ss.
XX
OS   Homo sapiens.
XX
PN   WO9820165-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US20313.
XX
PR   06-NOV-1996;   96US-0030455.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Hudson T,  Lander ES,  Wang D;
XX
DR   WPI; 1998-286974/25.
XX
PT   New isolated nucleic acid segments from the human genome - used for
PT   determining polymorphic forms for use in e.g. forensics, paternity
PT   testing or phenotypic typing for disease
XX
PS   Claim 1; Page 219; 310pp; English.
XX
CC   AAX10269-X12937 are human DNA fragments which contain biallelic
CC   polymorphic markers which have been isolated using the primers
CC   represented in AAX09121-X10268. The base occupying the polymorphic site
CC   is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC   can be used in methods for determining polymorphic forms in an individual
CC   for use in e.g. forensics, paternity testing or for phenotypic typing for
CC   diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
CC   syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC   familial hypercholesterolemia, polycystic kidney disease, hereditary
CC   spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC   haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC   syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC   autoimmune diseases, inflammation, cancer, diseases of the nervous
CC   system, infection by pathogenic microorganisms, and characteristics such
CC   as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC   endurance, fertility, and susceptibility or receptivity to particular
CC   drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC   segments can also be used to produce medicaments for the treatment or
CC   prophylaxis of such diseases.
XX
SQ   Sequence 201 BP; 32 A; 65 C; 62 G; 41 T; 1 other;

  Query Match             78.4%;  Score 40;  DB 19;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-11;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGG 40
              ||||||||||||||||||||||||||||||||||||||||
Db         90 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGG 129


RESULT 12
AAQ10907
ID   AAQ10907 standard; cDNA; 2393 BP.
XX
AC   AAQ10907;
XX
DT   25-MAR-2003  (updated)
DT   13-MAY-1991  (first entry)
XX
DE   40kD TNF inhibitor precursor gene in c40DK#6.
XX
KW   Tumour necrosis factor; inhibitor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             93..1478
FT                   /*tag=  a
XX
PN   AU9058976-A.
XX
PD   24-JAN-1991.
XX
PF   16-JUL-1990;   90AU-0058976.
XX
PR   07-FEB-1990;   90US-0479661.
PR   18-JUL-1989;   89US-0381080.
PR   11-DEC-1989;   89US-0450329.
```

```
XX
PA   (SYND ) SYNERGEN INC.
XX
DR   WPI; 1991-073847/11.
DR   P-PSDB; AAR11001.
XX
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
XX
PS   Disclosure; Fig 39; 142pp; English.
XX
CC   The sequence encodes the entire 40 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA.   The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also AAQ10878, AAQ10884 and AAQ10883.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 2393 BP; 484 A; 743 C; 738 G; 428 T; 0 other;

  Query Match             62.7%;  Score 32;  DB 12;  Length 2393;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-07;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db       1671 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1702


RESULT 13
AAC83951
ID   AAC83951 standard; DNA; 2394 BP.
XX
AC   AAC83951;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human 40 kDa TNF inhibitor precursor coding sequence.
XX
KW   TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW   IL-1; inflammatory disease; degenerative disease; human; lymphotoxin; ss.
XX
OS   Homo sapiens.
XX
PN   US6143866-A.
XX
PD   07-NOV-2000.
XX
PF   19-JAN-1995;   95US-0375242.
XX
PR   19-JUL-1990;   90US-0555274.
PR   09-JUL-1993;   93US-0090366.
PR   18-JUL-1989;   89US-0381080.
PR   11-DEC-1989;   89US-0450329.
PR   07-FEB-1990;   90US-0479661.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Squires C,  King MW,  Hale KK,  Brewer MT,  Thompson RC;
PI   Vanderslice RW,  Vannice J,  Kohno T;
XX
DR   WPI; 2001-006443/01.
DR   P-PSDB; AAB37686.
XX
PT   Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT   non-native cysteine residue cross-linked with polyethylene glycol,
PT   useful for treating inflammatory and degenerative diseases mediated by
PT   TNF  -
XX
PS   Example 12; Fig 39; 82pp; English.
XX
CC   The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC   (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC   novel TNF inhibitors of the present invention are useful as therapeutic
CC   agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC   for treating inflammatory and degenerative diseases mediated by TNF. The
CC   present sequence is the coding sequence for the precursor of 40 kDa TNF
CC   inhibitor. The 40 kDa TNF inhibitor can inhibit both TNF alpha and beta
CC   (lymphotoxin).
XX
SQ   Sequence 2394 BP; 484 A; 743 C; 738 G; 428 T; 1 other;

  Query Match             62.7%;  Score 32;  DB 22;  Length 2394;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-07;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db       1672 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1703


RESULT 14
AAL29880
ID   AAL29880 standard; DNA; 51 BP.
XX
AC   AAL29880;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #3088.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;   99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections -
XX
PS   Claim 1; Page 2271; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G-protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
```

```
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 51 BP; 11 A; 11 C; 20 G; 9 T; 0 other;

  Query Match             49.0%;  Score 25;  DB 22;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 0.00098;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTG 44
              |||||||||||||||||||||||||
Db         27 GGAAAGCCTCTGCTGCCATGGTGTG 51


RESULT 15
ABK33462
ID   ABK33462 standard; DNA; 23 BP.
XX
AC   ABK33462;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human TNF-receptor II 3'UNT nt 1690 (T/C) TET probe (T allele).
XX
KW   Human; anti-tumour necrosis factor receptor II; TNF receptor II;
KW   TNF receptor I; infliximab therapy; Crohn's disease; malignant disorder;
KW   inflammatory disorder; chronic disease; receptor; probe; ss.
XX
OS   Homo sapiens.
XX
PN   EP1172444-A1.
XX
PD   16-JAN-2002.
XX
PF   10-JUL-2000; 2000EP-0114786.
XX
PR   10-JUL-2000; 2000EP-0114786.
XX
PA   (CONA-) CONARIS RES INST GMBH.
XX
PI   Schreiber S,  Hampe J,  Mascheretti S;
XX
DR   WPI; 2002-156651/21.
XX
PT   Detecting non-responders to anti-human necrosis factor therapy,
PT   comprises testing an individual for homozygosity for a single
PT   nucleotide polymorphism in the gene coding for the tumour necrosis
PT   factor receptor II  -
XX
PS   Disclosure; Page 8; 45pp; English.
XX
CC   The present invention relates to a method for detecting non-responders
CC   to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC   an individual for homozygosity for at least one single nucleotide
CC   polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC   located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC   A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC   Met196Arg respectively, are also described. The method of the invention
CC   is useful for detecting non-responders to anti-TNF therapy such as
CC   infliximab therapy, or therapy of Crohn's disease. The genes containing
CC   the 2 novel polymorphisms are useful for diagnostic purposes in
CC   inflammatory, malignant or other chronic diseases. The present sequence
CC   represents a TaqMan probe used in the methods of the present invention.
XX
SQ   Sequence 23 BP; 1 A; 8 C; 6 G; 8 T; 0 other;

  Query Match             43.1%;  Score 22;  DB 24;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 0.038;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 CCTCTGCTGCCATGGTGTGTCC 47
              ||||||||||||||||||||||
Db          1 CCTCTGCTGCCATGGTGTGTCC 22


RESULT 16
AAQ10956
ID   AAQ10956 standard; DNA; 2339 BP.
XX
AC   AAQ10956;
XX
DT   09-JAN-2003  (updated)
DT   24-MAY-1991  (first entry)
XX
DE   Encodes human 75kD TNF-binding protein.
XX
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1179
FT                   /*tag=  a
FT                   /product= 75kD TNF-BP
XX
PN   EP417563-A.
XX
PD   20-MAR-1991.
XX
PF   31-AUG-1990;   90EP-0116707.
XX
PR   20-APR-1990;   90CH-0001347.
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
XX
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Lotscher H;
PI   Schlaeger EJ;
XX
DR   WPI; 1991-081851/12.
DR   P-PSDB; AAR11605.
XX
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
XX
PS   Claim 4; Fig 1; 26pp; German.
XX
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. Repeated sequencing showed a discrepancy
CC   at position 7 such that the third codon encodes either Thr or Ser.
CC   DNA constructs comprising the TNF-BP coding sequence may also
CC   contain a fragment encoding a human Ig domain. Recombinant
CC   constructs are used to transform cells to confer improved TNF-
CC   binding properties.
CC   See also AAQ10955.
CC   (Updated on 09-JAN-2003 to add missing OS field.)
XX
SQ   Sequence 2339 BP; 494 A; 720 C; 685 G; 439 T; 1 other;

  Query Match             41.2%;  Score 21;  DB 12;  Length 2339;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGG 40
              |||||||||||||||||||||
Db       1372 GGAAAGCCTCTGCTGCCATGG 1392
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```
RESULT 17
AAZ09171
ID   AAZ09171 standard; cDNA; 2339 BP.
XX
AC   AAZ09171;
XX
DT   20-MAR-2003  (updated)
DT   18-OCT-1999  (first entry)
XX
DE   Human tumour necrosis factor binding protein cDNA fragment.
XX
KW   Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KW   anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW   autoimmune glomerulonephritis; cerebral malaria; immune response;
KW   antagonist; diagnosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1179
FT                   /*tag=  a
FT                   /product= "TNF binding protein"
FT                   /note= "Partial sequence, no start codon given"
XX
PN   EP939121-A2.
XX
PD   01-SEP-1999.
XX
PF   31-AUG-1990;   99EP-0100703.
XX
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
PR   20-APR-1990;   90CH-0001347.
PR   31-AUG-1990;   90EP-0116707.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 1999-480840/41.
DR   P-PSDB; AAY30935.
XX
PT   New insoluble proteins, and fragments, that bind to tumor necrosis
PT   factor, used to treat e.g. septic shock or cerebral malaria
XX
PS   Claim 4a; Fig 4; 25pp; German.
XX
CC   This invention describes novel homogeneous insoluble proteins (I),
CC   their (in)soluble fragments (Ia) and their salts that can bind tumour
CC   necrosis factor (TNF). The products of the invention have
CC   anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC   to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC   glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC   (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC   diagnostic determination of TNF in body fluids. Antibodies raised against
CC   (I) are used for affinity purification of (I). This sequence encodes
CC   a tumour necrosis factor binding protein fragment described in the method
CC   of the invention.
CC   (Updated on 20-MAR-2003 to correct PF field.)
CC   (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ   Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;

  Query Match             41.2%;  Score 21;  DB 20;  Length 2339;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGG 40
              |||||||||||||||||||||
Db       1372 GGAAAGCCTCTGCTGCCATGG 1392
```

```
RESULT 18
AAH48860
ID   AAH48860 standard; DNA; 2339 BP.
XX
AC   AAH48860;
XX
DT   12-NOV-2001  (first entry)
XX
DE   Human TNFBP-associated DNA #2.
XX
KW   TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW   insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW   antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
KW   autoimmune glomerulonephritis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1179
FT                   /*tag=  a
FT                   /product= "TNFBP-associated protein"
XX
PN   EP1132471-A2.
XX
PD   12-SEP-2001.
XX
PF   31-AUG-1990; 2001EP-0108117.
XX
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
PR   20-APR-1990;   90CH-0001347.
PR   31-AUG-1990;   90EP-0116707.
PR   31-AUG-1990;   99EP-0100703.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 2001-559312/63.
DR   P-PSDB; AAB86818.
XX
PT   New homogeneous, insoluble proteins that bind tumor necrosis factor
PT   (TNF), useful for treating TNF-mediated disorders, e.g. inflammation -
XX
PS   Claim 4a; Fig 4; 26pp; German.
XX
CC   This invention describes novel insoluble proteins (I), also their
CC   (in)soluble fragments and pharmaceutically acceptable salts, able to bind
CC   tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC   invention have antiinflammatory, immunosuppressive, antibacterial,
CC   antiprotozoal activity. (I), and related recombinant proteins, are used
CC   to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC   sepsis; development of autoimmune glomerulonephritis and cerebral
CC   malaria. Also (I), or antibodies specific for them, are used for
CC   diagnostic determination of TNF in body fluids, for affinity purification
CC   of TNF and for identifying (ant)agonists of TNF. This sequence encodes a
CC   human TNF binding protein described in the method of the invention.
XX
SQ   Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;

  Query Match             41.2%;  Score 21;  DB 22;  Length 2339;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGG 40
              |||||||||||||||||||||
Db       1372 GGAAAGCCTCTGCTGCCATGG 1392


RESULT 19
```

ABQ74767
ID ABQ74767 standard; DNA; 15602 BP.
XX
AC ABQ74767;
XX
DT 24-OCT-2002 (first entry)
XX
DE Human TNFR2 partial genomic sequence SEQ ID NO:17.
XX
KW Tumour necrosis factor receptor 2; TNFR2; antisense oligonucleotide;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN US6410324-B1.
XX
PD 25-JUN-2002.
XX
PF 27-APR-2001; 2001US-0844634.
XX
PR 27-APR-2001; 2001US-0844634.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Watt AT;
XX
DR WPI; 2002-606814/65.
XX
PT New compounds antisense to nucleic acid encoding human or mouse tumor
PT necrosis factor receptor 2 are useful to treat disease associated with
PT mouse tumor necrosis factor receptor 2 expression -
XX
PS Claim 1; Column 67-80; 69pp; English.
XX
CC The present invention describes compounds of 8-30 nucleobases antisense
CC to a nucleic acid encoding human or mouse tumour necrosis factor
CC receptor 2 (TNFR2). Also described is a method for inhibiting expression
CC of human or mouse TNFR2 comprising contacting cells or tissues in vitro
CC with one of the claimed compounds. The antisense compounds are used to
CC treat a disease or condition associated with expression of TNFR2. The
CC present sequence represents a partial genomic sequence of human TNFR2,
CC which is used in an example from the present invention.
XX
SQ Sequence 15602 BP; 3439 A; 4290 C; 4227 G; 3646 T; 0 other;

Query Match 41.2%; Score 21; DB 24; Length 15602;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         20 GGAAAGCCTCTGCTGCCATGG 40
              |||||||||||||||||||||
Db      11202 GGAAAGCCTCTGCTGCCATGG 11222
```

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GenCore version 5.1.6

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Post-processing: Listing first 100 summaries

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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
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16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	51	100.0	2224	10	US-09-800-908-2	Sequence 2, Appli
3	51	100.0	2613	13	US-10-101-510-675	Sequence 675, App
4	51	100.0	3683	10	US-09-954-456-1187	Sequence 1187, Ap
5	51	100.0	3683	11	US-09-902-176A-49	Sequence 49, Appl
6	51	100.0	3683	11	US-09-902-176A-51	Sequence 51, Appl
7	51	100.0	3683	11	US-09-902-176A-53	Sequence 53, Appl
8	51	100.0	3683	13	US-10-101-510-22	Sequence 22, Appl
9	22	43.1	23	11	US-09-902-176A-46	Sequence 46, Appl
10	21	41.2	3492	15	US-10-207-655-191	Sequence 191, App

ALIGNMENTS

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RESULT 1
US-09-800-909-1
; Sequence 1, Application US/09800909
; Patent No. US20010019833A1
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BIGDA, Jacek
;    APPLICANT:  BELETSKY, Igor
;    APPLICANT:  METT, Igor
;    APPLICANT:  ENGELMANN, Hartmut
;    TITLE OF INVENTION:  TNF INHIBITORS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/800,909
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/476,862
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 94039
;      FILING DATE:  06-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 91229
;      FILING DATE:  06-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 90339
;      FILING DATE:  18-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=12A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2224 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1472
US-09-800-909-1

  Query Match             100.0%;  Score 51;  DB 9;  Length 2224;
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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 2
US-09-800-908-2
; Sequence 2, Application US/09800908
; Patent No. US20020111462A1
;  GENERAL INFORMATION:
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;       APPLICANT: WALLACH, David
;                  BIGDA, Jacek
;                  BELETSKY, Igor
;                  METT, Igor
;       TITLE OF INVENTION: TNF LIGANDS
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/800,908
;            FILING DATE: 08-Mar-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/477,347
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: IL 106271
;            FILING DATE: 08-JUL-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Townsend, G. Kevin
;            REGISTRATION NUMBER: 34,033
;            REFERENCE/DOCKET NUMBER: WALLACH=10
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;            TELEX: 248633
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2224 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  90..1472
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-800-908-2

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  Best Local Similarity   100.0%;  Pred. No. 6.8e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 3
US-10-101-510-675
; Sequence 675, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
;  APPLICANT: WAN, JACKSON
;  APPLICANT:  WANG, YIXIN
;  TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
;  FILE REFERENCE: 15117.0012
;  CURRENT APPLICATION NUMBER: US/10/101,510
;  CURRENT FILING DATE:  2002-03-20
;  PRIOR APPLICATION NUMBER: 60/276,947
;  PRIOR FILING DATE: 2001-03-20
;  NUMBER OF SEQ ID NOS: 805
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 675
;   LENGTH: 2613
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-101-510-675

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Db        580 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 630


RESULT 4
US-09-954-456-1187
; Sequence 1187, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Ca
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1187
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-1187

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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 5
US-09-902-176A-49
; Sequence 49, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
```

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;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (90)..(1475)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (156)
US-09-902-176A-49

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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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RESULT 6
US-09-902-176A-51
; Sequence 51, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (90)..(1475)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (156)
US-09-902-176A-51

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  Best Local Similarity   100.0%;  Pred. No. 6.3e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 7
US-09-902-176A-53
; Sequence 53, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (90)..(1475)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (156)
US-09-902-176A-53

  Query Match             100.0%;  Score 51;  DB 11;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 8
US-10-101-510-22
; Sequence 22, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
;  APPLICANT: WAN, JACKSON
;  APPLICANT:  WANG, YIXIN
;  TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
;  FILE REFERENCE: 15117.0012
;  CURRENT APPLICATION NUMBER: US/10/101,510
;  CURRENT FILING DATE:  2002-03-20
;  PRIOR APPLICATION NUMBER: 60/276,947
;  PRIOR FILING DATE: 2001-03-20
;  NUMBER OF SEQ ID NOS: 805
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-101-510-22

  Query Match             100.0%;  Score 51;  DB 13;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 9
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; Sequence 46, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
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;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: TET Probe#
US-09-902-176A-46

  Query Match             43.1%;  Score 22;  DB 11;  Length 23;
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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 CCTCTGCTGCCATGGTGTGTCC 47
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Db          1 CCTCTGCTGCCATGGTGTGTCC 22


RESULT 10
US-10-207-655-191
; Sequence 191, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 191
;   LENGTH: 3492
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-207-655-191

  Query Match             41.2%;  Score 21;  DB 15;  Length 3492;
  Best Local Similarity   100.0%;  Pred. No. 0.063;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1472 GGAAAGCCTCTGCTGCCATGG 1492


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Job time : 150 secs
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GenCore version 5.1.6

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Perfect score: 51
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 20

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	2224	3	US-08-477-347-2	Sequence 2, Appli
2	51	100.0	2224	3	US-08-476-862-1	Sequence 1, Appli
3	51	100.0	2224	4	US-09-800-909-1	Sequence 1, Appli
4	51	100.0	3683	4	US-09-844-634-3	Sequence 3, Appli
5	21	41.2	15602	4	US-09-844-634-17	Sequence 17, Appl

ALIGNMENTS

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RESULT 1
US-08-477-347-2
; Sequence 2, Application US/08477347
; Patent No. 6232446
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BIGDA, Jacek
;    APPLICANT:  BELETSKY, Igor
;    APPLICANT:  METT, Igor
;    TITLE OF INVENTION:  TNF LIGANDS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,347
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/115,685
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 106271
;      FILING DATE:  08-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, G. Kevin
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  WALLACH=10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2224 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1472
US-08-477-347-2

  Query Match            100.0%;  Score 51;  DB 3;  Length 2224;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 2
US-08-476-862-1
; Sequence 1, Application US/08476862
; Patent No. 6262239
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BIGDA, Jacek
;    APPLICANT:  BELETSKY, Igor
;    APPLICANT:  METT, Igor
;    APPLICANT:  ENGELMANN, Hartmut
;    TITLE OF INVENTION:  TNF INHIBITORS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,862
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 107267
;      FILING DATE:  12-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 94039
;      FILING DATE:  06-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 91229
;      FILING DATE:  06-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 90339
;      FILING DATE:  18-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=12A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2224 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1472
US-08-476-862-1

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  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 3
US-09-800-909-1
; Sequence 1, Application US/09800909
; Patent No. 6555111
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BIGDA, Jacek
;    APPLICANT:  BELETSKY, Igor
;    APPLICANT:  METT, Igor
;    APPLICANT:  ENGELMANN, Hartmut
;    TITLE OF INVENTION:  TNF INHIBITORS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/800,909
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/476,862
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 94039
;      FILING DATE:  06-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 91229
;      FILING DATE:  06-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 90339
;      FILING DATE:  18-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=12A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2224 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1472
US-09-800-909-1

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  Best Local Similarity   100.0%;  Pred. No. 2.6e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 4
US-09-844-634-3
; Sequence 3, Application US/09844634
; Patent No. 6410324
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRES
;  FILE REFERENCE: RTS-0216
;  CURRENT APPLICATION NUMBER: US/09/844,634
;  CURRENT FILING DATE:  2001-04-27
;  NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 3
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (90)...(1475)
US-09-844-634-3

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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 5
US-09-844-634-17
; Sequence 17, Application US/09844634
; Patent No. 6410324
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRES
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;  FILE REFERENCE: RTS-0216
;  CURRENT APPLICATION NUMBER: US/09/844,634
;  CURRENT FILING DATE:  2001-04-27
;  NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 17
;   LENGTH: 15602
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-844-634-17

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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      11202 GGAAAGCCTCTGCTGCCATGG 11222


Search completed: December 16, 2003, 20:28:33
Job time : 45 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 19:04:22 ; Search time 145 Seconds
(without alignments)
949.458 Million cell updates/sec

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Perfect score: 51
Sequence: 1 agcagaggcagcgagttggg.....ctgccatggtgtgtccctct 51

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 20

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	2224	16	AAQ89544	p75 Tumour Necrosi
2	51	100.0	2613	21	AAA49207	Human tumour necro
3	51	100.0	2613	24	ABZ35564	Human gene express
4	51	100.0	3683	24	ABZ34910	Human gene express
5	51	100.0	3683	24	ABQ74753	Human tumour necro
6	51	100.0	3683	24	ABK83997	Human cDNA differe
7	51	100.0	3683	24	ABL65877	Lung cancer relate
8	51	100.0	3683	24	ABK33465	Human TNF receptor
9	51	100.0	3683	24	ABK33466	Human TNF receptor
10	51	100.0	3683	24	ABK33467	Human TNF receptor
11	40	78.4	201	19	AAX12093	Human biallelic po
12	32	62.7	2393	12	AAQ10907	40kD TNF inhibitor
13	32	62.7	2394	22	AAC83951	Human 40 kDa TNF i
14	25	49.0	51	22	AAL29880	Human SNP oligonuc
15	22	43.1	23	24	ABK33462	Human TNF-receptor
16	21	41.2	2339	12	AAQ10956	Encodes human 75kD
17	21	41.2	2339	20	AAZ09171	Human tumour necro
18	21	41.2	2339	22	AAH48860	Human TNFBP-associ
19	21	41.2	15602	24	ABQ74767	Human TNFR2 partia

ALIGNMENTS

RESULT 1
AAQ89544
ID AAQ89544 standard; DNA; 2224 BP.
XX
AC AAQ89544;
XX
DT 25-MAR-2003 (updated)
DT 31-OCT-1995 (first entry)
XX
DE p75 Tumour Necrosis Factor Receptor.
XX
KW Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
KW receptor; ss..
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 90..1475
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FT /product= p75 TNF receptor.
FT misc_difference 1137..1139
FT /*tag= b
FT /transl_except= GCA encodes Glycine.
FT misc_difference 1140..1142
FT /*tag= c
FT /transl_except= CCA encodes Alanine.
FT misc_difference 1146..1148
FT /*tag= d
FT /transl_except= GTG encodes Glutamic acid.
FT misc_difference 1149..1151
FT /*tag= e
FT /transl_except= GAG encodes Alanine.
FT misc_difference 1152..1154
FT /*tag= f
FT /transl_except= GCC encodes Arginine.
FT misc_difference 1155..1157
FT /*tag= g
FT /transl_except= AGT encodes Alanine.
FT misc_difference 1158..1160
FT /*tag= h
FT /transl_except= GGG encodes Serine.
FT misc_difference 1161..1163
FT /*tag= i
FT /transl_except= GCC encodes Threonine.
FT misc_difference 1167..1169
FT /*tag= j
FT /transl_except= GAG encodes Serine.
FT misc_difference 1170..1172
FT /*tag= k
FT /transl_except= GCC encodes Serine.
FT misc_difference 1173..1175
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FT misc_difference 1176..1178
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FT /transl_except= GCC encodes Serine.
FT misc_difference 1182..1184

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FT                   /*tag=  n
FT                   /transl_except= ACC encodes Proline.
FT   misc_difference 1188..1190
FT                   /*tag=  o
FT                   /transl_except= AGC encodes Glycine.
FT   misc_difference 1191..1193
FT                   /*tag=  p
FT                   /transl_except= TCA encodes Histidine.
FT   misc_difference 1194..1196
FT                   /*tag=  q
FT                   /transl_except= GAT encodes Glycine.
FT   misc_difference 1197..1199
FT                   /*tag=  r
FT                   /transl_except= TCT encodes Threonine.
FT   misc_difference 2000..2002
FT                   /*tag=  s
FT                   /transl_except= TCC encodes Glutamine.
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FT   misc_difference 2006..2008
FT                   /*tag=  u
FT                   /transl_except= GGT encodes Proline.
FT   misc_difference 2012..2014
FT                   /*tag=  v
FT                   /transl_except= CAT encodes Valine.
FT   misc_difference 2015..2016
FT                   /*tag=  w
FT                   /transl_except= GGG encodes Glutamic acid.
FT   misc_difference 2017..2018
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FT   misc_difference 2019..2021
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FT                   /transl_except= CAG encodes Serine.
XX
PN   EP648783-A1.
XX
PD   19-APR-1995.
XX
PF   11-OCT-1994;   94EP-0116015.
XX
PR   12-OCT-1993;   93IL-0107267.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
PA   (WALL/) WALLACH D.
XX
PI   Beletsky I,  Bigda J,  Mett I,  Wallach D;
XX
DR   WPI; 1995-148673/20.
DR   P-PSDB; AAR72504.
XX
PT   Tumour necrosis factor (TNF) receptor ligand - used to increase
PT   inhibitory effect of a soluble TNF receptor
XX
PS   Disclosure; Figure 2; 18pp; English.
XX
CC   A ligand to a member of the tumour necrosis factor (TNF)/nerve
CC   growth factor (NGF) receptor family which binds either to the region
CC   of the 4th-Cys rich domain of the receptor, or to the region between
CC   it and the cell membrane may be used in the production of a
CC   pharmaceutical composition for increasing the inhibitory effect of a
CC   soluble receptor of the TNF/NGF receptor family.  This sequence
CC   encodes the p75 TNF receptor.  N in the sequence represents an
CC   unidentified nucleotide (poor reproduction in specification).
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2224 BP; 432 A; 697 C; 688 G; 400 T; 7 other;

  Query Match           100.0%;  Score 51;  DB 16;  Length 2224;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 2
AAA49207
ID   AAA49207 standard; DNA; 2613 BP.
XX
AC   AAA49207;
XX
DT   22-NOV-2000  (first entry)
XX
DE   Human tumour necrosis factor alpha receptor 2 gene exon 10.
XX
KW   Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;
KW   osteoporosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..2613
FT                   /*tag=  a
FT                   /product= "TNFR2"
FT                   /partial
FT   allele          replace (593,A), (598,G), (620,T)
FT                   /*tag=  b
FT                   /label= allele_1
FT   allele          replace (593,A), (598,T), (620,T)
FT                   /*tag=  c
FT                   /label= allele_2
FT   allele          replace (593,G), (598,T), (620,C)
FT                   /*tag=  d
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FT                   /label= allele_4
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FT                   /*tag=  f
FT                   /label= allele_5
XX
PN   WO200032826-A1.
XX
PD   08-JUN-2000.
XX
PF   30-NOV-1999;   99WO-US28403.
XX
PR   30-NOV-1998;   98US-0110268.
XX
PA   (UYDR-) UNIV DREXEL.
XX
PI   Spotila LD;
XX
DR   WPI; 2000-412362/35.
XX
PT   Identifying individuals at risk of developing osteoporosis comprises
PT   assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene
PT   in a DNA sample from an individual -
XX
PS   Claim 2; Page 17-18; 21pp; English.
XX
CC   The present sequence comprises exon 10 of the human tumour necrosis
CC   factor alpha receptor 2 (THFR2) gene. The sequence contains three
CC   polymorphic sites. By determining the genotype of an individual it is
CC   possible to identify those at risk of osteoporosis, which is
CC   characterised by low bone density and fragile bones, later in life. Those
CC   at greatest risk are those who possess allele 1, which is the rarest
CC   allele. This is particularly useful as many cases of osteoporosis go
CC   undetected at present.
XX
SQ   Sequence 2613 BP; 553 A; 750 C; 742 G; 568 T; 0 other;

  Query Match           100.0%;  Score 51;  DB 21;  Length 2613;
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  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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RESULT 3
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ID   ABZ35564 standard; cDNA; 2613 BP.
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AC   ABZ35564;
XX
DT   05-FEB-2003  (first entry)
XX
DE   Human gene expression profile polynucleotide SEQ ID NO 675.
XX
KW   Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW   bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW   tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW   gene expression; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200274979-A2.
XX
PD   26-SEP-2002.
XX
PF   20-MAR-2002; 2002WO-US08456.
XX
PR   20-MAR-2001; 2001US-276947P.
XX
PA   (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI   Wan J,  Wang Y;
XX
DR   WPI; 2002-740862/80.
XX
PT   New gene expression profile generated from primary, endothelial,
PT   epithelial, and muscle cell types, useful for identifying disease
PT   pathologies involving alterations of gene expression, e.g. cancer  -
XX
PS   Example 3; Page 798-799; 850pp; English.
XX
CC   The invention relates to a gene expression profile comprising one or more
CC   genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
CC   is a coronary artery endothelium, umbilical artery or vein endothelium,
CC   aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC   endothelium, myometrium microvascular endothelium, keratinocyte
CC   epithelium, bronchial epithelium, mammary epithelium, prostate
CC   epithelium, renal cortical epithelium, renal proximal tubule epithelium,
CC   small airway epithelium, renal epithelium, umbilical artery smooth
CC   muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
CC   dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
CC   aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
CC   bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
CC   osteoblasts or prostate stromal cell. The gene expression profile is used
CC   for determining the level of RNA expression for a sample, determining the
CC   phenotype of a cell and distinguishing cell types. The gene or a protein
CC   expression profile is useful in identifying disease pathologies
CC   involving alterations of gene expression. The assessment of expression
CC   profiles may provide meaningful information with respect to tumour type
CC   and stage, treatment methods, and prognosis. The gene or protein
CC   expression profile may also be used for creating microarrays. The
CC   microarray is useful for genetic and physical mapping of genomes, DNA
CC   sequencing, genetic or medical diagnosis, genotyping of organisms,
CC   confirming cell or tissue identifications and in identifying promising
CC   antibiotics, antiviral or antifungal agents.
XX
SQ   Sequence 2613 BP; 553 A; 750 C; 742 G; 568 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 2613;
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  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db        580 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 630


RESULT 4
ABZ34910
ID   ABZ34910 standard; cDNA; 3683 BP.
XX
AC   ABZ34910;
XX
DT   05-FEB-2003  (first entry)
XX
DE   Human gene expression profile polynucleotide SEQ ID NO 22.
XX
KW   Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW   bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW   tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW   gene expression; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200274979-A2.
XX
PD   26-SEP-2002.
XX
PF   20-MAR-2002; 2002WO-US08456.
XX
PR   20-MAR-2001; 2001US-276947P.
XX
PA   (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI   Wan J,  Wang Y;
XX
DR   WPI; 2002-740862/80.
XX
PT   New gene expression profile generated from primary, endothelial,
PT   epithelial, and muscle cell types, useful for identifying disease
PT   pathologies involving alterations of gene expression, e.g. cancer  -
XX
PS   Claim 1; Page 235-236; 850pp; English.
XX
CC   The invention relates to a gene expression profile comprising one or more
CC   genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
CC   is a coronary artery endothelium, umbilical artery or vein endothelium,
CC   aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC   endothelium, myometrium microvascular endothelium, keratinocyte
CC   epithelium, bronchial epithelium, mammary epithelium, prostate
CC   epithelium, renal cortical epithelium, renal proximal tubule epithelium,
CC   small airway epithelium, renal epithelium, umbilical artery smooth
CC   muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
CC   dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
CC   aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
CC   bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
CC   osteoblasts or prostate stromal cell. The gene expression profile is used
CC   for determining the level of RNA expression for a sample, determining the
CC   phenotype of a cell and distinguishing cell types. The gene or a protein
CC   expression profile is useful in identifying disease pathologies
CC   involving alterations of gene expression. The assessment of expression
CC   profiles may provide meaningful information with respect to tumour type
CC   and stage, treatment methods, and prognosis. The gene or protein
CC   expression profile may also be used for creating microarrays. The
CC   microarray is useful for genetic and physical mapping of genomes, DNA
CC   sequencing, genetic or medical diagnosis, genotyping of organisms,
CC   confirming cell or tissue identifications and in identifying promising
CC   antibiotics, antiviral or antifungal agents.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 5
ABQ74753
ID   ABQ74753 standard; cDNA; 3683 BP.
XX
AC   ABQ74753;
XX
DT   24-OCT-2002  (first entry)
XX
DE   Human tumour necrosis factor receptor 2 encoding cDNA SEQ ID NO:3.
XX
KW   Tumour necrosis factor receptor 2; TNFR2; antisense oligonucleotide;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "tumour necrosis factor receptor 2"
XX
PN   US6410324-B1.
XX
PD   25-JUN-2002.
XX
PF   27-APR-2001; 2001US-0844634.
XX
PR   27-APR-2001; 2001US-0844634.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Watt AT;
XX
DR   WPI; 2002-606814/65.
DR   P-PSDB; ABP52451.
XX
PT   New compounds antisense to nucleic acid encoding human or mouse tumor
PT   necrosis factor receptor 2 are useful to treat disease associated with
PT   mouse tumor necrosis factor receptor 2 expression  -
XX
PS   Claim 1; Column 53-58; 69pp; English.
XX
CC   The present invention describes compounds of 8-30 nucleobases antisense
CC   to a nucleic acid encoding human or mouse tumour necrosis factor
CC   receptor 2 (TNFR2). Also described is a method for inhibiting expression
CC   of human or mouse TNFR2 comprising contacting cells or tissues in vitro
CC   with one of the claimed compounds. The antisense compounds are used to
CC   treat a disease or condition associated with expression of TNFR2. The
CC   present sequence encodes human TNFR2, which is used in an example from
CC   the present invention.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 6
ABK83997
ID   ABK83997 standard; cDNA; 3683 BP.
XX
AC   ABK83997;
XX
DT   14-AUG-2002  (first entry)
XX
DE   Human cDNA differentially expressed in granulocytic cells #568.
XX
KW   Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW   viral infection; parasitic infection; protozoal infection;
KW   fungal infection; sterile inflammatory disease; psoriasis;
KW   rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW   cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW   adult respiratory distress syndrome; inflammatory bowel disease;
KW   Crohn's disease; ulcerative colitis; periodontal disease;
KW   granulocyte activation; chronic inflammation; allergy.
XX
OS   Homo sapiens.
XX
PN   WO200228999-A2.
XX
PD   11-APR-2002.
XX
PF   03-OCT-2001; 2001WO-US30821.
XX
PR   03-OCT-2000; 2000US-237189P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Beazer-Barclay Y,  Weissman SM,  Yamaga S,  Vockley J;
XX
DR   WPI; 2002-435328/46.
XX
PT   Detecting granulocyte activation by detecting differential expression
PT   of genes associated with granulocyte activation, which serves as
PT   diagnostic markers that is useful for monitoring disease states and
PT   drug toxicity  -
XX
PS   Claim 1; SEQ ID No 568; 114pp; English.
XX
CC   The invention relates to detecting (M1) granulocyte (GC) activation
CC   (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC   DNA chip analysis as given in the specification, and comparing
CC   the expression level to an expression level in an unactivated
CC   GC, where differential expression of Gs is indicative of GCA.
CC   Also included are modulating (M2) GA by contacting GC with an agent
CC   that alters the expression of at least one gene in Gs; (2) screening (M3)
CC   for an agent capable of modulating GCA or an inflammation (especially
CC   chronic) in a tissue, an allergic response in a subject, exposure of a
CC   subject to a pathogen or sterile inflammatory disease using the
CC   gene expression profile; (3) detecting (M4) an inflammation (especially
CC   chronic) in a tissue, an allergic response in a subject, exposure of a
CC   subject to a pathogen or sterile inflammatory disease, by detecting the
CC   level of expression in a sample of the tissue of gene(s) from Gs, where
CC   the level of expression of the gene is indicative of inflammation;
CC   (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC   an allergic response in a subject, exposure of a subject to a pathogen
CC   or sterile inflammatory disease, by contacting a tissue having
CC   inflammation with an agent that modulates the expression of gene(s)
CC   from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC   modulating GA; M3 is useful for screening an agent capable of modulating
CC   GCA preferably in an inflammation in a tissue; M4 is useful for
CC   detecting an inflammation (especially chronic) in a tissue, an allergic
CC   response in a subject, exposure of a subject to a pathogen or sterile
CC   inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC   glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC   reperfusion injury, ARDS, adult respiratory distress syndrome,
CC   inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC   periodontal disease; also bacterial infection, viral infection,
CC   parasitic infection, protozoal infection, fungal infection and M5 is
CC   useful for treating one of the above conditions. The present
CC   sequence represents a gene differentially expressed in granulocytes.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
```

```
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 7
ABL65877
ID   ABL65877 standard; DNA; 3683 BP.
XX
AC   ABL65877;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Lung cancer related gene sequence SEQ ID NO:4214.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US10838.
XX
PR   05-JUN-2000; 2000US-209473P.
PR   05-JUN-2000; 2000US-209531P.
PR   18-SEP-2000; 2000US-233133P.
PR   18-SEP-2000; 2000US-233617P.
PR   20-SEP-2000; 2000US-234009P.
PR   20-SEP-2000; 2000US-234034P.
PR   20-SEP-2000; 2000US-234052P.
PR   22-SEP-2000; 2000US-234509P.
PR   22-SEP-2000; 2000US-234567P.
PR   25-SEP-2000; 2000US-234923P.
PR   25-SEP-2000; 2000US-234924P.
PR   25-SEP-2000; 2000US-235077P.
PR   25-SEP-2000; 2000US-235082P.
PR   25-SEP-2000; 2000US-235134P.
PR   25-SEP-2000; 2000US-235280P.
PR   26-SEP-2000; 2000US-235637P.
PR   26-SEP-2000; 2000US-235638P.
PR   27-SEP-2000; 2000US-235711P.
PR   27-SEP-2000; 2000US-235720P.
PR   27-SEP-2000; 2000US-235840P.
PR   27-SEP-2000; 2000US-235863P.
PR   28-SEP-2000; 2000US-236028P.
PR   28-SEP-2000; 2000US-236032P.
PR   28-SEP-2000; 2000US-236033P.
PR   28-SEP-2000; 2000US-236034P.
PR   28-SEP-2000; 2000US-236109P.
PR   28-SEP-2000; 2000US-236111P.
PR   29-SEP-2000; 2000US-236842P.
PR   29-SEP-2000; 2000US-236891P.
PR   02-OCT-2000; 2000US-237172P.
PR   02-OCT-2000; 2000US-237173P.
PR   02-OCT-2000; 2000US-237278P.
PR   02-OCT-2000; 2000US-237294P.
PR   02-OCT-2000; 2000US-237295P.
PR   02-OCT-2000; 2000US-237316P.
PR   03-OCT-2000; 2000US-237425P.
PR   03-OCT-2000; 2000US-237598P.
PR   03-OCT-2000; 2000US-237604P.
PR   03-OCT-2000; 2000US-237606P.
PR   03-OCT-2000; 2000US-237608P.
PR   01-NOV-2000; 2000US-244867P.
PR   01-NOV-2000; 2000US-245084P.
XX
PA   (AVAL-) AVALON PHARM.
XX
PI   Young PE,  Augustus M,  Carter KC,  Ebner R,  Endress G,  Horrigan S;
PI   Soppet DR,  Weaver Z;
XX
DR   WPI; 2002-188264/24.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a
PT   chemical agent to be tested for anti-neoplastic activity, and
PT   determining a change in expression of a gene of a signature gene set  -
XX
PS   Claim 1; SEQ ID 4214; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an
CC   anti-neoplastic agent. The method involves exposing cells to a chemical
CC   agent to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening
CC   an anti-neoplastic agent, and can be used for producing a product which
CC   is the data collected with respect to the anti-neoplastic agent as a
CC   result of M1, and the data is sufficient to convey the chemical
CC   structure and/or properties of the agent. M1 can be used in the
CC   treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC   oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC   adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC   infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC   carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 8
ABK33465
ID   ABK33465 standard; DNA; 3683 BP.
XX
AC   ABK33465;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human TNF receptor II gene.
XX
KW   Human; anti-tumour necrosis factor receptor II; TNF receptor II;
KW   chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW   inflammatory disorder; chronic disease; receptor; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "TNF receptor II"
FT   sig_peptide     90..155
FT                   /*tag=  b
FT   mat_peptide     156..1472
FT                   /*tag=  c
XX
```

```
PN   EP1172444-A1.
XX
PD   16-JAN-2002.
XX
PF   10-JUL-2000; 2000EP-0114786.
XX
PR   10-JUL-2000; 2000EP-0114786.
XX
PA   (CONA-) CONARIS RES INST GMBH.
XX
PI   Schreiber S,  Hampe J,  Mascheretti S;
XX
DR   WPI; 2002-156651/21.
DR   P-PSDB; AAU75172.
XX
PT   Detecting non-responders to anti-human necrosis factor therapy,
PT   comprises testing an individual for homozygosity for a single
PT   nucleotide polymorphism in the gene coding for the tumour necrosis
PT   factor receptor II  -
XX
PS   Disclosure; Page 23-27; 45pp; English.
XX
CC   The present invention relates to a method for detecting non-responders
CC   to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC   an individual for homozygosity for at least one single nucleotide
CC   polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC   located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC   A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC   Met196Arg respectively, are also described. The method of the invention
CC   is useful for detecting non-responders to anti-TNF therapy such as
CC   infliximab therapy, or therapy of Crohn's disease. The genes containing
CC   the 2 novel polymorphisms are useful for diagnostic purposes in
CC   inflammatory, malignant or other chronic diseases. The present sequence
CC   encodes for human TNF receptor II.
XX
SQ   Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 9
ABK33466
ID   ABK33466 standard; DNA; 3683 BP.
XX
AC   ABK33466;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human TNF receptor II gene with SNP in exon 2.
XX
KW   Human; anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
KW   chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW   inflammatory disorder; chronic disease; receptor; gene;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "TNF receptor II variant #1"
FT   sig_peptide     90..155
FT                   /*tag=  b
FT   mat_peptide     156..1472
FT                   /*tag=  c
FT   variation       replace (257, A)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   EP1172444-A1.
XX
PD   16-JAN-2002.
XX
PF   10-JUL-2000; 2000EP-0114786.
XX
PR   10-JUL-2000; 2000EP-0114786.
XX
PA   (CONA-) CONARIS RES INST GMBH.
XX
PI   Schreiber S,  Hampe J,  Mascheretti S;
XX
DR   WPI; 2002-156651/21.
DR   P-PSDB; AAU75173.
XX
PT   Detecting non-responders to anti-human necrosis factor therapy,
PT   comprises testing an individual for homozygosity for a single
PT   nucleotide polymorphism in the gene coding for the tumour necrosis
PT   factor receptor II  -
XX
PS   Claim 15; Page 29-33; 45pp; English.
XX
CC   The present invention relates to a method for detecting non-responders
CC   to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC   an individual for homozygosity for at least one single nucleotide
CC   polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC   located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC   A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC   Met196Arg respectively, are also described. The method of the invention
CC   is useful for detecting non-responders to anti-TNF therapy such as
CC   infliximab therapy, or therapy of Crohn's disease. The genes containing
CC   the 2 novel polymorphisms are useful for diagnostic purposes in
CC   inflammatory, malignant or other chronic diseases. The present sequence
CC   represents the human TNF receptor II gene containing the SNP in exon 2.
XX
SQ   Sequence 3683 BP; 780 A; 1098 C; 1087 G; 718 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 10
ABK33467
ID   ABK33467 standard; DNA; 3683 BP.
XX
AC   ABK33467;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human TNF receptor II gene with SNP in exon 6.
XX
KW   Human; anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
KW   chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW   inflammatory disorder; chronic disease; receptor; gene;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..1475
FT                   /*tag=  a
FT                   /product= "TNF receptor II variant #2"
FT   sig_peptide     90..155
FT                   /*tag=  b
FT   mat_peptide     156..1472
FT                   /*tag=  c
```

```
FT   variation       replace (676, T)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   EP1172444-A1.
XX
PD   16-JAN-2002.
XX
PF   10-JUL-2000; 2000EP-0114786.
XX
PR   10-JUL-2000; 2000EP-0114786.
XX
PA   (CONA-) CONARIS RES INST GMBH.
XX
PI   Schreiber S,  Hampe J,  Mascheretti S;
XX
DR   WPI; 2002-156651/21.
DR   P-PSDB; AAU75174.
XX
PT   Detecting non-responders to anti-human necrosis factor therapy,
PT   comprises testing an individual for homozygosity for a single
PT   nucleotide polymorphism in the gene coding for the tumour necrosis
PT   factor receptor II  -
XX
PS   Claim 16; Page 35-39; 45pp; English.
XX
CC   The present invention relates to a method for detecting non-responders
CC   to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC   an individual for homozygosity for at least one single nucleotide
CC   polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC   located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC   A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC   Met196Arg respectively, are also described. The method of the invention
CC   is useful for detecting non-responders to anti-TNF therapy such as
CC   infliximab therapy, or therapy of Crohn's disease. The genes containing
CC   the 2 novel polymorphisms are useful for diagnostic purposes in
CC   inflammatory, malignant or other chronic diseases. The present sequence
CC   represents the human TNF receptor II gene containing the SNP in exon 6.
XX
SQ   Sequence 3683 BP; 780 A; 1098 C; 1088 G; 717 T; 0 other;

  Query Match             100.0%;  Score 51;  DB 24;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-17;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 11
AAX12093
ID   AAX12093 standard; DNA; 201 BP.
XX
AC   AAX12093;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Human biallelic polymorphic DNA fragment M32315b.
XX
KW   Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW   detection; phenotypic typing; characteristic; infection; hereditary;
KW   autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW   treatment; marker; ss.
XX
OS   Homo sapiens.
XX
PN   WO9820165-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US20313.
XX
PR   06-NOV-1996;   96US-0030455.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Hudson T,  Lander ES,  Wang D;
XX
DR   WPI; 1998-286974/25.
XX
PT   New isolated nucleic acid segments from the human genome - used for
PT   determining polymorphic forms for use in e.g. forensics, paternity
PT   testing or phenotypic typing for disease
XX
PS   Claim 1; Page 219; 310pp; English.
XX
CC   AAX10269-X12937 are human DNA fragments which contain biallelic
CC   polymorphic markers which have been isolated using the primers
CC   represented in AAX09121-X10268. The base occupying the polymorphic site
CC   is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC   can be used in methods for determining polymorphic forms in an individual
CC   for use in e.g. forensics, paternity testing or for phenotypic typing for
CC   diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
CC   syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC   familial hypercholesterolemia, polycystic kidney disease, hereditary
CC   spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC   haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC   syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC   autoimmune diseases, inflammation, cancer, diseases of the nervous
CC   system, infection by pathogenic microorganisms, and characteristics such
CC   as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC   endurance, fertility, and susceptibility or receptivity to particular
CC   drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC   segments can also be used to produce medicaments for the treatment or
CC   prophylaxis of such diseases.
XX
SQ   Sequence 201 BP; 32 A; 65 C; 62 G; 41 T; 1 other;

  Query Match             78.4%;  Score 40;  DB 19;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-11;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGG 40
              ||||||||||||||||||||||||||||||||||||||||
Db         90 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGG 129


RESULT 12
AAQ10907
ID   AAQ10907 standard; cDNA; 2393 BP.
XX
AC   AAQ10907;
XX
DT   25-MAR-2003  (updated)
DT   13-MAY-1991  (first entry)
XX
DE   40kD TNF inhibitor precursor gene in c40DK#6.
XX
KW   Tumour necrosis factor; inhibitor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             93..1478
FT                   /*tag=  a
XX
PN   AU9058976-A.
XX
PD   24-JAN-1991.
XX
PF   16-JUL-1990;   90AU-0058976.
XX
PR   07-FEB-1990;   90US-0479661.
PR   18-JUL-1989;   89US-0381080.
PR   11-DEC-1989;   89US-0450329.
```

```
XX
PA   (SYND ) SYNERGEN INC.
XX
DR   WPI; 1991-073847/11.
DR   P-PSDB; AAR11001.
XX
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
XX
PS   Disclosure; Fig 39; 142pp; English.
XX
CC   The sequence encodes the entire 40 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd. from RNA form U937 cells treated with PMA/PHA.   The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also AAQ10878, AAQ10884 and AAQ10883.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 2393 BP; 484 A; 743 C; 738 G; 428 T; 0 other;

  Query Match             62.7%;  Score 32;  DB 12;  Length 2393;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-07;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db       1671 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1702


RESULT 13
AAC83951
ID   AAC83951 standard; DNA; 2394 BP.
XX
AC   AAC83951;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human 40 kDa TNF inhibitor precursor coding sequence.
XX
KW   TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW   IL-1; inflammatory disease; degenerative disease; human; lymphotoxin; ss.
XX
OS   Homo sapiens.
XX
PN   US6143866-A.
XX
PD   07-NOV-2000.
XX
PF   19-JAN-1995;   95US-0375242.
XX
PR   19-JUL-1990;   90US-0555274.
PR   09-JUL-1993;   93US-0090366.
PR   18-JUL-1989;   89US-0381080.
PR   11-DEC-1989;   89US-0450329.
PR   07-FEB-1990;   90US-0479661.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Squires C,  King MW,  Hale KK,  Brewer MT,  Thompson RC;
PI   Vanderslice RW,  Vannice J,  Kohno T;
XX
DR   WPI; 2001-006443/01.
DR   P-PSDB; AAB37686.
XX
PT   Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT   non-native cysteine residue cross-linked with polyethylene glycol,
PT   useful for treating inflammatory and degenerative diseases mediated by
PT   TNF  -
XX
PS   Example 12; Fig 39; 82pp; English.
XX
CC   The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC   (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC   novel TNF inhibitors of the present invention are useful as therapeutic
CC   agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC   for treating inflammatory and degenerative diseases mediated by TNF. The
CC   present sequence is the coding sequence for the precursor of 40 kDa TNF
CC   inhibitor. The 40 kDa TNF inhibitor can inhibit both TNF alpha and beta
CC   (lymphotoxin).
XX
SQ   Sequence 2394 BP; 484 A; 743 C; 738 G; 428 T; 1 other;

  Query Match             62.7%;  Score 32;  DB 22;  Length 2394;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-07;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              ||||||||||||||||||||||||||||||||
Db       1672 GGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1703


RESULT 14
AAL29880
ID   AAL29880 standard; DNA; 51 BP.
XX
AC   AAL29880;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #3088.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;   99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections -
XX
PS   Claim 1; Page 2271; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G-protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
```

```
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 51 BP; 11 A; 11 C; 20 G; 9 T; 0 other;

  Query Match            49.0%;  Score 25;  DB 22;  Length 51;
  Best Local Similarity  100.0%;  Pred. No. 0.00098;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGGTGTG 44
              |||||||||||||||||||||||||
Db         27 GGAAAGCCTCTGCTGCCATGGTGTG 51


RESULT 15
ABK33462
ID   ABK33462 standard; DNA; 23 BP.
XX
AC   ABK33462;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human TNF-receptor II 3'UNT nt 1690 (T/C) TET probe (T allele).
XX
KW   Human; anti-tumour necrosis factor receptor II; TNF receptor II;
KW   TNF receptor I; infliximab therapy; Crohn's disease; malignant disorder;
KW   inflammatory disorder; chronic disease; receptor; probe; ss.
XX
OS   Homo sapiens.
XX
PN   EP1172444-A1.
XX
PD   16-JAN-2002.
XX
PF   10-JUL-2000; 2000EP-0114786.
XX
PR   10-JUL-2000; 2000EP-0114786.
XX
PA   (CONA-) CONARIS RES INST GMBH.
XX
PI   Schreiber S,  Hampe J,  Mascheretti S;
XX
DR   WPI; 2002-156651/21.
XX
PT   Detecting non-responders to anti-human necrosis factor therapy,
PT   comprises testing an individual for homozygosity for a single
PT   nucleotide polymorphism in the gene coding for the tumour necrosis
PT   factor receptor II  -
XX
PS   Disclosure; Page 8; 45pp; English.
XX
CC   The present invention relates to a method for detecting non-responders
CC   to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC   an individual for homozygosity for at least one single nucleotide
CC   polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC   located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC   A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC   Met196Arg respectively, are also described. The method of the invention
CC   is useful for detecting non-responders to anti-TNF therapy such as
CC   infliximab therapy, or therapy of Crohn's disease. The genes containing
CC   the 2 novel polymorphisms are useful for diagnostic purposes in
CC   inflammatory, malignant or other chronic diseases. The present sequence
CC   represents a TaqMan probe used in the methods of the present invention.
XX
SQ   Sequence 23 BP; 1 A; 8 C; 6 G; 8 T; 0 other;

  Query Match            43.1%;  Score 22;  DB 24;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 0.038;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 CCTCTGCTGCCATGGTGTGTCC 47
              ||||||||||||||||||||||
Db          1 CCTCTGCTGCCATGGTGTGTCC 22


RESULT 16
AAQ10956
ID   AAQ10956 standard; DNA; 2339 BP.
XX
AC   AAQ10956;
XX
DT   09-JAN-2003  (updated)
DT   24-MAY-1991  (first entry)
XX
DE   Encodes human 75kD TNF-binding protein.
XX
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1179
FT                   /*tag=  a
FT                   /product= 75kD TNF-BP
XX
PN   EP417563-A.
XX
PD   20-MAR-1991.
XX
PF   31-AUG-1990;   90EP-0116707.
XX
PR   20-APR-1990;   90CH-0001347.
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
XX
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Lotscher H;
PI   Schlaeger EJ;
XX
DR   WPI; 1991-081851/12.
DR   P-PSDB; AAR11605.
XX
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
XX
PS   Claim 4; Fig 1; 26pp; German.
XX
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. Repeated sequencing showed a discrepancy
CC   at position 7 such that the third codon encodes either Thr or Ser.
CC   DNA constructs comprising the TNF-BP coding sequence may also
CC   contain a fragment encoding a human Ig domain. Recombinant
CC   constructs are used to transform cells to confer improved TNF-
CC   binding properties.
CC   See also AAQ10955.
CC   (Updated on 09-JAN-2003 to add missing OS field.)
XX
SQ   Sequence 2339 BP; 494 A; 720 C; 685 G; 439 T; 1 other;

  Query Match            41.2%;  Score 21;  DB 12;  Length 2339;
  Best Local Similarity  100.0%;  Pred. No. 0.12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGG 40
              |||||||||||||||||||||
Db       1372 GGAAAGCCTCTGCTGCCATGG 1392
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```
RESULT 17
AAZ09171
ID   AAZ09171 standard; cDNA; 2339 BP.
XX
AC   AAZ09171;
XX
DT   20-MAR-2003  (updated)
DT   18-OCT-1999  (first entry)
XX
DE   Human tumour necrosis factor binding protein cDNA fragment.
XX
KW   Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KW   anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW   autoimmune glomerulonephritis; cerebral malaria; immune response;
KW   antagonist; diagnosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1179
FT                   /*tag=  a
FT                   /product= "TNF binding protein"
FT                   /note= "Partial sequence, no start codon given"
XX
PN   EP939121-A2.
XX
PD   01-SEP-1999.
XX
PF   31-AUG-1990;   99EP-0100703.
XX
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
PR   20-APR-1990;   90CH-0001347.
PR   31-AUG-1990;   90EP-0116707.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 1999-480840/41.
DR   P-PSDB; AAY30935.
XX
PT   New insoluble proteins, and fragments, that bind to tumor necrosis
PT   factor, used to treat e.g. septic shock or cerebral malaria
XX
PS   Claim 4a; Fig 4; 25pp; German.
XX
CC   This invention describes novel homogeneous insoluble proteins (I),
CC   their (in)soluble fragments (Ia) and their salts that can bind tumour
CC   necrosis factor (TNF). The products of the invention have
CC   anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC   to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC   glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC   (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC   diagnostic determination of TNF in body fluids. Antibodies raised against
CC   (I) are used for affinity purification of (I). This sequence encodes
CC   a tumour necrosis factor binding protein fragment described in the method
CC   of the invention.
CC   (Updated on 20-MAR-2003 to correct PF field.)
CC   (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ   Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;

  Query Match             41.2%;  Score 21;  DB 20;  Length 2339;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGG 40
               |||||||||||||||||||||
Db       1372 GGAAAGCCTCTGCTGCCATGG 1392
```

```
RESULT 18
AAH48860
ID   AAH48860 standard; DNA; 2339 BP.
XX
AC   AAH48860;
XX
DT   12-NOV-2001  (first entry)
XX
DE   Human TNFBP-associated DNA #2.
XX
KW   TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW   insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW   antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
KW   autoimmune glomerulonephritis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1179
FT                   /*tag=  a
FT                   /product= "TNFBP-associated protein"
XX
PN   EP1132471-A2.
XX
PD   12-SEP-2001.
XX
PF   31-AUG-1990; 2001EP-0108117.
XX
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
PR   20-APR-1990;   90CH-0001347.
PR   31-AUG-1990;   90EP-0116707.
PR   31-AUG-1990;   99EP-0100703.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 2001-559312/63.
DR   P-PSDB; AAB86818.
XX
PT   New homogeneous, insoluble proteins that bind tumor necrosis factor
PT   (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
XX
PS   Claim 4a; Fig 4; 26pp; German.
XX
CC   This invention describes novel insoluble proteins (I), also their
CC   (in)soluble fragments and pharmaceutically acceptable salts, able to bind
CC   tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC   invention have antiinflammatory, immunosuppressive, antibacterial,
CC   antiprotozoal activity. (I), and related recombinant proteins, are used
CC   to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC   sepsis; development of autoimmune glomerulonephritis and cerebral
CC   malaria. Also (I), or antibodies specific for them, are used for
CC   diagnostic determination of TNF in body fluids, for affinity purification
CC   of TNF and for identifying (ant)agonists of TNF. This sequence encodes a
CC   human TNF binding protein described in the method of the invention.
XX
SQ   Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;

  Query Match             41.2%;  Score 21;  DB 22;  Length 2339;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGG 40
               |||||||||||||||||||||
Db       1372 GGAAAGCCTCTGCTGCCATGG 1392

RESULT 19
```

ABQ74767
ID ABQ74767 standard; DNA; 15602 BP.
XX
AC ABQ74767;
XX
DT 24-OCT-2002 (first entry)
XX
DE Human TNFR2 partial genomic sequence SEQ ID NO:17.
XX
KW Tumour necrosis factor receptor 2; TNFR2; antisense oligonucleotide;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN US6410324-B1.
XX
PD 25-JUN-2002.
XX
PF 27-APR-2001; 2001US-0844634.
XX
PR 27-APR-2001; 2001US-0844634.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Watt AT;
XX
DR WPI; 2002-606814/65.
XX
PT New compounds antisense to nucleic acid encoding human or mouse tumor
PT necrosis factor receptor 2 are useful to treat disease associated with
PT mouse tumor necrosis factor receptor 2 expression -
XX
PS Claim 1; Column 67-80; 69pp; English.
XX
CC The present invention describes compounds of 8-30 nucleobases antisense
CC to a nucleic acid encoding human or mouse tumour necrosis factor
CC receptor 2 (TNFR2). Also described is a method for inhibiting expression
CC of human or mouse TNFR2 comprising contacting cells or tissues in vitro
CC with one of the claimed compounds. The antisense compounds are used to
CC treat a disease or condition associated with expression of TNFR2. The
CC present sequence represents a partial genomic sequence of human TNFR2,
CC which is used in an example from the present invention.
XX
SQ Sequence 15602 BP; 3439 A; 4290 C; 4227 G; 3646 T; 0 other;

Query Match 41.2%; Score 21; DB 24; Length 15602;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 GGAAAGCCTCTGCTGCCATGG 40
||||||||||||||||||||
Db 11202 GGAAAGCCTCTGCTGCCATGG 11222

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Job time : 145 secs

GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	2224	9	US-09-800-909-1	Sequence 1, Appli
2	51	100.0	2224	10	US-09-800-908-2	Sequence 2, Appli
3	51	100.0	2613	13	US-10-101-510-675	Sequence 675, App
4	51	100.0	3683	10	US-09-954-456-1187	Sequence 1187, Ap
5	51	100.0	3683	11	US-09-902-176A-49	Sequence 49, Appl
6	51	100.0	3683	11	US-09-902-176A-51	Sequence 51, Appl
7	51	100.0	3683	11	US-09-902-176A-53	Sequence 53, Appl
8	51	100.0	3683	13	US-10-101-510-22	Sequence 22, Appl
9	22	43.1	23	11	US-09-902-176A-46	Sequence 46, Appl
10	21	41.2	3492	15	US-10-207-655-191	Sequence 191, App

ALIGNMENTS

RESULT 1
US-09-800-909-1
; Sequence 1, Application US/09800909
; Patent No. US20010019833A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; APPLICANT: ENGELMANN, Hartmut
; TITLE OF INVENTION: TNF INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,909
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,862
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 94039
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 91229
; FILING DATE: 06-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 90339
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=12A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
US-09-800-909-1

Query Match 100.0%; Score 51; DB 9; Length 2224;
Best Local Similarity 100.0%; Pred. No. 6.8e-18;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700
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RESULT 2
US-09-800-908-2
; Sequence 2, Application US/09800908
; Patent No. US20020111462A1
; GENERAL INFORMATION:

```
;       APPLICANT: WALLACH, David
;                  BIGDA, Jacek
;                  BELETSKY, Igor
;                  METT, Igor
;       TITLE OF INVENTION: TNF LIGANDS
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/800,908
;            FILING DATE: 08-Mar-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/477,347
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: IL 106271
;            FILING DATE: 08-JUL-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Townsend, G. Kevin
;            REGISTRATION NUMBER: 34,033
;            REFERENCE/DOCKET NUMBER: WALLACH=10
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;            TELEX: 248633
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2224 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  90..1472
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-800-908-2

  Query Match             100.0%;  Score 51;  DB 10;  Length 2224;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 3
US-10-101-510-675
; Sequence 675, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
;  APPLICANT: WAN, JACKSON
;  APPLICANT:  WANG, YIXIN
;  TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
;  FILE REFERENCE: 15117.0012
;  CURRENT APPLICATION NUMBER: US/10/101,510
;  CURRENT FILING DATE:  2002-03-20
;  PRIOR APPLICATION NUMBER: 60/276,947
;  PRIOR FILING DATE: 2001-03-20
;  NUMBER OF SEQ ID NOS: 805
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 675
;   LENGTH: 2613
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-101-510-675

  Query Match             100.0%;  Score 51;  DB 13;  Length 2613;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 630


RESULT 4
US-09-954-456-1187
; Sequence 1187, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1187
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-1187

  Query Match             100.0%;  Score 51;  DB 10;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 5
US-09-902-176A-49
; Sequence 49, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
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;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
;    LENGTH: 3683
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (90)..(1475)
;    FEATURE:
;    NAME/KEY: mat_peptide
;    LOCATION: (156)
US-09-902-176A-49

  Query Match             100.0%;  Score 51;  DB 11;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 6
US-09-902-176A-51
; Sequence 51, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
;    LENGTH: 3683
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (90)..(1475)
;    FEATURE:
;    NAME/KEY: mat_peptide
;    LOCATION: (156)
US-09-902-176A-51

  Query Match             100.0%;  Score 51;  DB 11;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 7
US-09-902-176A-53
; Sequence 53, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
;    LENGTH: 3683
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (90)..(1475)
;    FEATURE:
;    NAME/KEY: mat_peptide
;    LOCATION: (156)
US-09-902-176A-53

  Query Match             100.0%;  Score 51;  DB 11;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 8
US-10-101-510-22
; Sequence 22, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
;  APPLICANT: WAN, JACKSON
;  APPLICANT:  WANG, YIXIN
;  TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
;  FILE REFERENCE: 15117.0012
;  CURRENT APPLICATION NUMBER: US/10/101,510
;  CURRENT FILING DATE:  2002-03-20
;  PRIOR APPLICATION NUMBER: 60/276,947
;  PRIOR FILING DATE: 2001-03-20
;  NUMBER OF SEQ ID NOS: 805
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;    LENGTH: 3683
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-101-510-22

  Query Match             100.0%;  Score 51;  DB 13;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 9
US-09-902-176A-46
; Sequence 46, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
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;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: TET Probe#
US-09-902-176A-46

  Query Match             43.1%;  Score 22;  DB 11;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 0.043;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 CCTCTGCTGCCATGGTGTGTCC 47
              ||||||||||||||||||||||
Db          1 CCTCTGCTGCCATGGTGTGTCC 22


RESULT 10
US-10-207-655-191
; Sequence 191, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 191
;   LENGTH: 3492
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-207-655-191

  Query Match             41.2%;  Score 21;  DB 15;  Length 3492;
  Best Local Similarity   100.0%;  Pred. No. 0.063;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GGAAAGCCTCTGCTGCCATGG 40
              |||||||||||||||||||||
Db       1472 GGAAAGCCTCTGCTGCCATGG 1492


Search completed: December 16, 2003, 21:05:26
Job time : 150 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 19:40:17 ; Search time 45 Seconds
(without alignments)
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Title: US-09-856-937A-1_COPY_580_630
Perfect score: 51
Sequence: 1 agcagaggcagcgagttggg.....ctgccatggtgtgtccctct 51

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 20

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	2224	3	US-08-477-347-2	Sequence 2, Appli
2	51	100.0	2224	3	US-08-476-862-1	Sequence 1, Appli
3	51	100.0	2224	4	US-09-800-909-1	Sequence 1, Appli
4	51	100.0	3683	4	US-09-844-634-3	Sequence 3, Appli
5	21	41.2	15602	4	US-09-844-634-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-477-347-2
; Sequence 2, Application US/08477347
; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,347
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/115,685
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
US-08-477-347-2

Query Match 100.0%; Score 51; DB 3; Length 2224;
Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db 1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700

RESULT 2
US-08-476-862-1
; Sequence 1, Application US/08476862
; Patent No. 6262239
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; APPLICANT: ENGELMANN, Hartmut
; TITLE OF INVENTION: TNF INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,862
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 107267
;      FILING DATE:  12-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 94039
;      FILING DATE:  06-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 91229
;      FILING DATE:  06-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 90339
;      FILING DATE:  18-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=12A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2224 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1472
US-08-476-862-1

  Query Match             100.0%;  Score 51;  DB 3;  Length 2224;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
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Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 3
US-09-800-909-1
; Sequence 1, Application US/09800909
; Patent No. 6555111
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BIGDA, Jacek
;    APPLICANT:  BELETSKY, Igor
;    APPLICANT:  METT, Igor
;    APPLICANT:  ENGELMANN, Hartmut
;    TITLE OF INVENTION:  TNF INHIBITORS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/800,909
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/476,862
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 94039
;      FILING DATE:  06-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 91229
;      FILING DATE:  06-AUG-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IL 90339
;      FILING DATE:  18-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  WALLACH=12A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2224 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..1472
US-09-800-909-1

  Query Match             100.0%;  Score 51;  DB 4;  Length 2224;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 4
US-09-844-634-3
; Sequence 3, Application US/09844634
; Patent No. 6410324
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRESSI
;  FILE REFERENCE: RTS-0216
;  CURRENT APPLICATION NUMBER: US/09/844,634
;  CURRENT FILING DATE:  2001-04-27
;  NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 3
;   LENGTH: 3683
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (90)...(1475)
US-09-844-634-3

  Query Match             100.0%;  Score 51;  DB 4;  Length 3683;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-18;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 AGCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCT 1700


RESULT 5
US-09-844-634-17
; Sequence 17, Application US/09844634
; Patent No. 6410324
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRESSI
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;  FILE REFERENCE: RTS-0216
;  CURRENT APPLICATION NUMBER: US/09/844,634
;  CURRENT FILING DATE:  2001-04-27
;  NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 17
;   LENGTH: 15602
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-844-634-17

  Query Match             41.2%;  Score 21;  DB 4;  Length 15602;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          20 GGAAAGCCTCTGCTGCCATGG 40
               |||||||||||||||||||||
Db       11202 GGAAAGCCTCTGCTGCCATGG 11222


Search completed: December 16, 2003, 20:28:33
Job time : 45 secs
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